

## FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCTCGGGGATCCTCTAGAGATCCCTCGACCTCGA  
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG  
CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG  
CTGCTGCCGCCCCGCGCCGGAGGCCGCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGCT  
GGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCGGGAACA  
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCGCTGCTGGAGATC  
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGGCGCAGGAGGA  
GCACCTGGAGGCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTCGAGTGGTTTT  
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC  
CAGGGCGGATCCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA  
GGGCGACGGGTCTTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG  
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC  
TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCGAGTGTGAAGTGGGCTGGGTGCT  
GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG  
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG  
GGCTGCACAGGGGAAGGCCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA  
CGGACAGTGTGCAGATGTGGACGAGTGCTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG  
AAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTGTCTGACGGCTTCGAAGAAACG  
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT  
GCCCTCCCGCGAAGACCTGTAATGTGCGCGGACTTACCCTTTAAATTATTGAGAAGGATGTCC  
CGTGGAATAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGCGGGGAGAGGCTGC  
CTGCTCTCTAACGGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA  
AACAGACTTGTATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTGTAGGTAATCAGG  
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC  
TTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCA  
TCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAACTC  
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCGCAGCACCATGGCCTGAAAT  
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTTCTGAGGCGGAAAGAACCAGCTGTGGAATG  
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC  
ATCTCAATTAGTCAGCAACCCAGTTTT

[illegible]

><MW: 38192, pI: 4.53, NX(S/T): 2

**Signal peptide:**

**N-glycosylation sites.**

Glycosaminoglycan attachment sites.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

### Casein kinase II phosphorylation sites.

**Tyrosine kinase phosphorylation site.**

N-myristoylation sites.

Aspartic acid and asparagine hydroxylation site.

EGF-like domain cysteine pattern signature.

Leucine zipper pattern.

amino acids 94-116

### FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC  
GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGTCTAAACGGGAACA  
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG  
GCACGAGGAGTTTTCCCCGGCAGCGAGGAGGTCTTGAGCAGCATGGCCCCGGAGGAGCGCCTTC  
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC  
CGGGCCGCCGAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA  
TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT  
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC  
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCCTGTCTTGGCTCCCTGGATA  
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA  
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAACAGGATGGGGTGGCAGCATTTGAAGT  
GGATGTGATTGTTATGAATTCGAAGGCAACACCATTCTCCAAACACCTCAAAATGCTATCT  
TCTTTAAACATGTCAACAAGCTGAGTGCCCGAGGCGGGTGCCGAAATGGAGGCTTTTGTAAT  
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTTG  
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG  
GATTCTATGGAGTGAAGTGTGACAAAGCAAAGTCTCAACCACCTGCTTTAATGGAGGGACC  
TGTTTCTACCCTGGAAAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG  
CAAATGCCCACAACCCTGTGCAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGTT  
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGCACAT  
GGAACCTGCCATGAACCCAAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA  
TAAAAGGTACGAAGCCAGCCTCATACTGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC  
ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG  
TGAACTCCGACATCTGAAACGTTTTAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCA  
TGTGTTGAATGTTCAAATAATGTTCACTTAAAGTAACTGGCCTGAATTTTATTAGCT  
TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTTAAAGTTTCTAAGTACGTCTGTAG  
CATGATGGTATAGATTTTCTGTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA  
TCAGGTAAAAATTTTCAGTGTGTAGTTGGCAGATATTTTCAAAATTACAATGCATTTATGGT  
GTCTGGGGGCAGGGGAACATCAGAAAGGTTAAATTGGGCAAAAATGCGTAAGTCACAAGAAT  
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAATTTTATGTCAGATATTTAGAT  
GTTTGTACATTTTTTAAAAATTGCTCTTAATTTTTTAACTCTCAATACAATATATTTTGACC  
TTACCATTATTCCAGAGATTCACTATTAATAAAAAAAAAAATTACACTGTGGTAGTGGCATT  
AAACAATATAATATATTTCTAAACACAATGAAATAGGGAATATAATGTATGAACTTTTTGACAT  
TGGCTTGAAGCAATATAATATATTGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT  
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTAGTTTTTTGGAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGCTTGGC  
CGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

[illegible]

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><subunit 1 of 1, 379 aa, 0 stop
```

MARRSAFPAAALWLSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK  
MAPFTHDFRKAQQORMPAIPVNIHSMNFTWQAAGQAEYFYEFSLRSLDKGIMADPTVNVPLL  
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNLILQTPQNAIFFKTCQQAECPPGC  
RNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST  
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPVC  
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP  
PESNYIW

amino acids 1-28

## amino acids 88-92, 245-249

## amino acids 319-323

## amino acids 370-378

amino acids 184-190, 185-191, 189-195, 315-321

## amino acids 285-293

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

## FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG  
CCCCAGCCCCACACCTTCACCAGGGGCCAGGAGCCACCATGTTGGCGATGTCCACTGGGGCTAC  
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCCAGCAGGGTCGTGGGCGCCGG  
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGGTACTGCCAGGA  
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT  
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC  
TGCCTCGGCGTGCCACCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCGTATCTA  
TCCAGTCTTGGGAACGTACTGGGACAACCTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT  
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG  
GAACCACAGCGCCTTCTGGGGCATGACCCTGGATGAGGGCATTTCGCTACCGCCTGGGCACCA  
TCCGCCCATCTTCCTCGGTTCATGAACATGCATGAAATTTATACAGTGCTGAACCCAGGGGAG  
GTGCTTCCACAGCCTTCGAGGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGA  
CCAAGGCAACTGTGCAGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT  
CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCCAAGAACCTGCTGTCTTGTGAC  
ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCG  
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC  
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC  
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT  
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA  
TGGAGGTGCATGAGGACTTCTTCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC  
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG  
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC  
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGAG  
AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTTCATCACTGAGGCTG  
CGGGCACACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGGCCCCAATG  
GGGCGGTGACCCAGCCTCGCCGACAGAGCCCGGGGCGCAGGCGGGCGCCAGGGCGCTAAT  
CCCGGCGCGGGTTCCGCTGACGCAGCGCCCCGCTGGGAGCCGCGGGCAGGCGAGACTGGCG  
GAGCCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG  
ATCCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC  
CCCAATACCCCAACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG  
TTGCCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTCA  
AGTGACCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCACCACACCTGGC  
TAATTTTTGTATTTTTTGTAAGAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC  
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCCTCCCAAAGTGCTGGGATTGCAGGCATGAGCC  
ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA  
TAAAACCAAAGTATTGATAAAAAAAA

## **FIGURE 6**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC  
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTYWDNCNR  
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

### **N-glycosylation site.**

amino acids 78-82, 161-165

### **Casein kinase II phosphorylation site.**

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,  
411-415

### **N-myristoylation site.**

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,  
269-275, 378-384, 442-448

### **Amidation site.**

amino acids 26-30, 318-322

### **Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 398-409

[illegible]

AGGCTCCTTGGCCCTTTTTCCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATCCA  
ATTCTCTTGGGACACATNACGCCTGTCCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC  
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG  
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC  
CCCCCTGTATGATGCACAGCCGAGCCATGGGTCTGGGGCAAGCGCCAGGCCACTGCCCACTGC  
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACCTCCTGTCTACCGCCTCGGCTC  
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG  
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG  
AGGCCAGAGAGATAACCGCCGGCATGGGACCCACTCAG

*[The page contains faint, illegible markings or bleed-through from the reverse side.]*

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT  
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG  
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTC  
CAGCTTGAACCTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT  
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT  
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG  
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG  
GCCAGTGGGAGCCTGTCCTGGTTCTTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT  
CTGCACCCCTGTCCCCACCCTGACCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA  
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCCTCCAACCCTCTCTGCTGCTGTTTC  
CATGGCCCAGCATTTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT  
CCCTGCCCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA  
GGGGACAGGCACTCAGGAGGGGCCAGTTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA  
GGACAAGAGTCGACGTGAGTTCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA  
GGGGCCAGGCCTCACATTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT  
AATAAACACCTGTTGGATAAGCCAAAAAAA

## **FIGURE 9**

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPPLRCSLHSACCSGDPASYRLWGAPLQPT  
LGVVPQASVPLLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPDPPMALSRTPTRQISSDT  
DPPADGPSNPLCCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

### **Signal peptide:**

amino acids 1-47

### **N-glycosylation site.**

amino acids 31-35, 74-78, 84-88

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 76-80

### **N-myristoylation site.**

amino acids 56-60

### **Amidation site.**

amino acids 70-74

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Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

CCCACGCGTCCGAACCTCTCCAGCGATGGGGAGCCGCCCGCCTGCTGCCAACCTCACTCTGT  
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC  
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA  
CGTGCAAGTCAACGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC  
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTCGCATCAAAGGGGCTGAGAGTGAGAAG  
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAGACTG  
CGTGTTACGGAGATCGTGCTGGAGAACAACTATACGGCCTTCCAGAACGCCCCGGCACGAGG  
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAAC  
CAGCGCGAGGCCCACCTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCACGC  
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACC CGCCGACCAAGCGCACAC  
GGCGGCCCCAGCCCCTCACGTAGTCTCTGGGAGGCAGGGGGCAGCAGCCCCTGGGCGCGCCTCCC  
CACCCCTTTCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC  
GAGGGAGGACCCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTG  
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT  
GAGTGTCACCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC  
CGCTGAAAGGTCAGCGACTGAAGGCCTTGCAAGACAACCGTCTGGAGGTGGCTGTCCTCAAAA  
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCCAGCCCCAACTCCTCCTGGCTAGACTGTA  
GGAAGGGACTTTTGTGGTTTGTGGTTTGTGGTTTCAGGAAAAAAGAAAGGGAGAGAGAGGAAAATAG  
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCCACCCCCAACTCCAGCCC  
CGGAATAAAACCATTTTTCCTGC

## **FIGURE 11**

MGAARLLPNLTLCLQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLENNYTAFQONARHEGWFMATRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

### **Signal peptide:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 9-13, 126-130

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 60-64

### **Casein kinase II phosphorylation site.**

amino acids 65-69

### **Tyrosine kinase phosphorylation site.**

amino acids 39-48, 89-97

### **N-myristoylation site.**

amino acids 69-75, 188-194

### **Amidation site.**

amino acids 58-62

### **HBGF/FGF family signature.**

amino acids 103-128

## FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG  
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC  
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT  
CATTTTGATTTTGCTGTTTATTTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTAT  
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCCAGCCATGGGGCTTTTTTCTT  
GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAACTCCTGGCCTGCC  
CTAGTGTGTGCCGCTGCGACAGGAACTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG  
CCTCTTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC  
TGGATTTCCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC  
AACTGGACGAATTCCCATGAACCTTCCCAAGAATGTCAGAGTTCTCCATTGTCAGGAAAAC  
AATATTACAGACATTTACGGGCTGCTCTTGCCCAGCTCTTGAAGCTTGAAGAGCTGCACCT  
GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC  
TCAAATTGTTGTTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC  
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTATATCCGACATGGCCTTCCAGAA  
TCTCACGAGCTTGGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG  
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC  
CACCTCTCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTTGCAGGACAACCAGAT  
AAACCACATTTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA  
ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC  
ACTGCTCGGAATAACCCTTGGTTTTGTGACTGCAGTATTAAATGGGTACAGAATGGCTCAA  
ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGGTCTGAACAAGTCGGG  
GGATGGCCGTGAGGGAATTAATAATGAATCTTTTGTCTGTCCACCACGACCCCCGGCCTG  
CCTCTCTTACCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCCACCCTCTCTAT  
TCCAAACCCTAGCAGAAGCTACACGCCTCCAACTCCTACCACATCGAACTTCCCACGATTC  
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC  
CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTACCGTGATGGCATA  
CAAACCTCACATGGGTGAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTCAGGAGCGCATAG  
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT  
TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCATTTGTTTCAGAGGC  
CACCACCCATGCCTCCTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA  
CGTCCCACAGCATGGGCTCCCCCTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT  
GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGCTGGCATATGCACAAAAGGGGCGCTACACCTC  
CCAGAAGTGGAATAACAACGGGGCCGGCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA  
AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTTTCAGATCGTCTCCTTAAATAACGAT  
CAACTCCTTAAAGGAGATTTACAGCTGCAGCCCATTTACACCCCAAATGGGGGCATTAATTA  
CACAGACTGCCATATCCCCAACAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC  
ACTGCCATACGTGAAGCAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA  
CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT  
TTGTGCATTTGAATACTCTGTAATTTATACGGTGTACTATATAATGGGATTTAAAAAAGTG  
CTATCTTTTCTATTTCAAGTTAATTACAAACAGTTTTTGTAACCTTTTGCTTTTTTAAATCTT

## **FIGURE 13**

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP  
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI  
SRAALAQLLKLEELHLDNNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR  
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD  
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN  
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMVRELNMNLLSCPTTTPGLPLFTP  
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPTIPDWDGRERVTPPISERIQLSIHFVND  
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL  
DAFNRYAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL  
LSVFCWHMHKKGRYTSQKWYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLKG  
DFRLQPIYTPNGGINYTDCHIPNMMRYCNSSVPDLEHCHT

### **Signal peptide:**

amino acids 1-42

### **Transmembrane domain:**

amino acids 542-561

### **N-glycosylation site.**

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

### **Tyrosine kinase phosphorylation site.**

amino acids 319-328

### **N-myristoylation site.**

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,  
522-528, 545-551, 633-639

### **Amidation site.**

amino acids 581-585

### **Leucine zipper pattern.**

amino acids 164-186

### **Phospholipase A2 aspartic acid active site.**

amino acids 39-50

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Species	Sex	Age	Weight (g)	Length (mm)	Wing (mm)	Tail (mm)	Culmen (mm)	Tarsus (mm)	Middle toe (mm)	Claw (mm)
1. <i>Alcedo corbula</i>	♂	Ad.	10.5	110	55	45	15	18	12	5
2. <i>Alcedo corbula</i>	♀	Ad.	10.0	105	50	40	14	17	11	4
3. <i>Alcedo corbula</i>	♂	Ad.	10.2	108	52	42	14.5	17.5	11.5	4.5
4. <i>Alcedo corbula</i>	♀	Ad.	9.8	102	48	38	13.5	16.5	10.5	4
5. <i>Alcedo corbula</i>	♂	Ad.	10.1	106	51	41	14.2	17.2	11.2	4.8
6. <i>Alcedo corbula</i>	♀	Ad.	9.9	104	49	39	13.8	16.8	10.8	4.2
7. <i>Alcedo corbula</i>	♂	Ad.	10.3	109	53	43	14.8	17.8	11.8	5.2
8. <i>Alcedo corbula</i>	♀	Ad.	9.7	101	47	37	13.2	16.2	10.2	3.8
9. <i>Alcedo corbula</i>	♂	Ad.	10.4	111	54	44	15.2	18.2	12.2	5.4
10. <i>Alcedo corbula</i>	♀	Ad.	9.6	100	46	36	13.0	16.0	10.0	3.6

ACTTTGGAGCAAGCGGGCGGGCGGGAGACAGAGGCGAGAGGCGAAGCTGGGGCTCCGTCCTCGCCTCCACACGAGCG  
ATCCCCGAGGAGAGCCGCGGCCCTCGGCGAGGGCGAAGAGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCCCTGCC  
TCGCTTCCCAGGCGCCGGCGGGCTGCAGCCTTGCCCCCTCTTGCTCGCCTTGAAAAATGGAAGATGCTCGCAGGCCT  
GCTTTTCTGCTGATCCTCGGACAGATCGTCTCCTCCTCGCCGAGGCCAGGGAGCGGTACAGTGGGAGGTCCATCT  
CTAGGGCGAGACACGCTCGGACCCACCCGACAGCGGCCCTTCGGAGAGTTCCTGTGAGAACAGCGGGCAGACC  
TGGTTTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCCATGACTATGCAAGGTTCAAGGAGTTCATCGTGGACA  
TCTTGCAATTCTTGACATTGGTCTGTATGTACCCGAGTGGGCCGTGCTCCAATATGGCAGCAGTGTCAAGAAATG  
AGTTCTCCCTCAAGACCTTCAAGAGGAAGTCCGAGGTGGAGCGTGTGTCAAGAGGATGCGGCATCTGTCCACGG  
GCACCATGATGTGGGCTGGCCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGGCCCGGCCCTGA  
GGGAGAATGTGCCACGGGTATAATGATCGTGACAGATGGGAGACCTCAGGACTCCGTGGCCGAGGTGGCTGCTA  
AGGCACGGGACACGGGCATCCTAATCTTTGCCATTGGTGTGGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG  
GGAGTGAGCCCCATGAGGACCATGTCTTCTTGTGGCCAAATTCAGCCAGATTGAGACGCTGACCTCCGTGTTTCC  
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCCCTGGAGCATAACTGTGCCCACTTCTGCATCAACATCCCTG  
GCTCATACGTCTGCAGGTGCAACAAAGGCTACATTTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTGT  
GTGCCATGGGAGACCACAACCTGTGAGCAGCTCTGTGTGAATGTGCCGGGCTCCTTCGTCTGCCAGTGTCTACAGTG  
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGTGGCTGTGGACTACTGTGCCTCAGAAAAACACGGATGTGAAC  
ATGAGTGTGTAATGTCTGATGGTCTTACCTTTGCGAGTGCCATGAAGGATTGTCTTTAAACCCAGATGAAAAA  
CGTGCACAAGGATCAACTACTGTGCACGTGAACAAACCGGGCTGTGAGCATGAGTGTGCTCAACATGGAGGAGACT  
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAGCCGAGTGGACCACTGTGCAC  
AGCAGGACCATGGCTGTGAGCAGCTGTGTCTGAACACGGAGGATTCTTTCGTCTGCCAGTGTCTCAGAAGGCTTCC  
TCATCAACGAGGACCTCAAGACCTGCTCCCGGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCCT  
GTCTCAACATGGACAGATCCTTTGGCTGTCACTGTCTGAGGACACCTGCTCCGACCGGATGGGAAGACGTGTG  
CAAAATTTGGAATCTTTGTGCTCTGGGGGACCACGGTTGTGAACATTCTGTGTGAAGCAGTGAAGATTCTTTGTGT  
GCCAGTGTCTTTGAAGTTATATACTCCGTGAAGATGGA AAAACCTGCAGAAGGAAAGATGTCTGCCAAGCTATAG  
ACCATGGCTGTGAACACATTTGTGTGAACAGTGACGACTCATACACGTGCGAGTGTCTTGAGGGGATTCCGGCTCG  
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGCGAACACATTTGTGTTA  
ATAATGGGAATTTACATCTGCAAAATGCTCAGAGGGGATTTGTTCTAGCTGAGGACGGAAGACGGTGCAAGAAAT  
GCACGTGAAGGCCCAATTGACCTGGTCTTTGTGATCGATGATCAAGAGTCTTGAGAGAAGAGAAATTTTGAGTTCG  
TGAAGCAGTTTGTCACTGGAATTATAGATTCTTTGACAATTTCCCCCAAAGCCGCTGAGTGGGGCTGCTCCAGT  
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACTTCAACTCAGCCAAAGACATGAAAAAAGCCGTGGCCC  
ACATGAAATACATGGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTTGAGAGAAAGTTTACCCAAG  
GAGAAGGGGCCAGGCCCCCTTCCACAAGGGTGCCACAGCAGCCATTGTGTTTACCACGAGCGGGCTCAGGATG  
ACGTCTCCGATGGGCGAGTAAGCTTCAAGGCCAAGGCCAATGGTATCATATGTATGCTGTTGGGGTAGGAAAAGCCATTG  
AGGAGGAATCAAGAGATTGCTCTGAGCCCAACAAACAGCATCTCTTATGCTGGGGAAGACTTCAGCACAATGG  
ATGAGATAAGTGAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCAG  
CAGGGGAACCTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCCAGTACCATAAATATCCAAGACCTACTTT  
CCTGTTCTAATTTTGCAGTGCAACACAGATATCTGTTTGAAGAAGACAATCTTTTACGGTCTACACAAAAGCTTT  
CCCATTCAACAAAACCTTCAGGAAGCCCTTTGGAAGAAAAACAGCATCAATGCAAAATGTGAAAACCTTATAATGT  
TCCAGAACCTTGCAACGAAGAGTTAAGAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC  
TGGAAAATCGCCTGAGATACAGATGAAGATTAGAAATCGCGACACATTTGTAGTCAATTGTATCAGGATTAACAAT  
GAACGCAGTGCAGAGCCCCAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAAAACAATCAGTACTGA  
GAAACCTGGTTTGGCCACAGAACAAAGACAAGAAGTATACATAACTTGTATAAAATTTATCTAGGAAAAAAATCCT  
TCAAGAAATCTAAGATGAATTTACAGGTTGAGAATGAATAAGCTATGCAAGGTATTTTGTAAATATACTGTGGACAC  
AATFTGCTTCTGCCCTCATCTGCCCTTAGTGTGCAATCTCACTTGTACTATCAGATAAAGTTTGCACAGTCTTACTT  
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTGTGACTGGACTTACCTTGATATGTATATGTATGTATG  
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTTGGATTTTTTATACAATATTAATAATTCACCACTTCAG

## **FIGURE 15**

MEKMLAGCFLILGQIVLLPAEARERSRGRSISRGRHARTHPTALLESSCENKRADLVFII  
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV  
KMRHLSTGTMTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD  
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN  
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA  
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCINTRINYCALNKPGC  
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLLI  
NEDLKTC SRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSDGKTC AKLDS CALGDHGCE  
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA  
EDGKRCRRKDVCSTHHGCEHICVNNGNSYICKCSEGFVLAEDGRCKKCTEGPIDLVFVID  
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA  
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN  
GITMYAVGVGKAIEEELQEIASEPTNKHLYAEDFSTMDIEISEKLKKGICEALEDSDGRQDS  
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL  
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMALENRLRYR

### **Signal peptide:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 221-225

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 115-119, 606-610, 892-896

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,  
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,  
781-785, 819-823, 866-870

### **N-myristoylation site.**

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,  
639-645, 690-696, 752-758, 792-798

### **Amidation site.**

amino acids 314-318, 560-564, 601-605

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,  
540-546, 581-587

## **FIGURE 16**

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGGCAGCCTCG  
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGGAGGGC  
CATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA  
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACCTGCCCCGCAACCGGTTGCAG  
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC  
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC  
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC  
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA  
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT  
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCCAT  
GTGGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA  
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTCATCCGTG  
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC  
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC  
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC  
TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC  
ATTGCTCCCCGGACCTGCCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCTT  
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCCAGGCCTGGTGCAT  
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT  
GGGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGGTTTTCTTCCTCTGGCTTGAGCCG  
CATGGGTGCTGTGCCTGTGATGGTGCCCTGCCCAGAGTCAAGCTGGCTCTCTGGTATGATGAC  
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCCTATAAGGGTCACCTCTAGCAC  
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC  
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA  
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG  
CTGAAATTAGCTACTACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC  
CCCCTTGATCTGTACCCACCCCTATCTAACACCACCCTTGGCTCCCACTCCAGCTCCCTGT  
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTC  
TTATTAAAATAACATGAAATATGTGTTGTTTTTCATTTGCAAATTTAAATAAAGATACATAA  
TGTTTGTATGAAAAA

## **FIGURE 17**

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS  
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY  
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCQSPRSKPAVQYQ  
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA  
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL  
SSVTSARALRPPHGPPrPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR  
MGAVPVMVPAQSQAGSLV

### **Signal peptide:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 245-267

### **N-glycosylation site.**

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

### **N-myristoylation site.**

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,  
262-268, 308-314, 363-369, 364-370

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 164-175

## FIGURE 18

[illegible]

## **FIGURE 19**

MKRLPLLVVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC  
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVCIAA  
NINKTLTKIRSIKEPVALLOEVYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL  
SNSTLTETVKTVNNFVQRDTFVVWDKLSVNHRRTHLTKLMHTVEQATLRISQSFQKTTEFDT  
NSTDIALKVFFFDSDYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS  
SSDNFLKPKQNYDNSEEEERVISVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF  
WNYSPTMNGSWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG  
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCIIAGL  
LHYFFLAFAWMCIEGHLVYLVVGVYINKGFLHKNFYIFGYLSPAVVVGFSALGYRYYGT  
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRTAGLKPEVSCFENIRSCARGA  
LALLFLLGTTWIFGVLVHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV  
PCCFGCLR

### **Signal peptide:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,  
648-664

### **N-glycosylation site.**

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,  
188-192, 249-253, 381-385, 395-399

### **Glycosaminoglycan attachment site.**

amino acids 49-53

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 360-364

### **Casein kinase II phosphorylation site.**

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,  
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,  
346-350, 608-612

### **Tyrosine kinase phosphorylation site.**

amino acids 36-44, 669-677, 670-678

### **N-myristoylation site.**

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,  
434-440, 480-486, 521-527

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 75-87

## **FIGURE 20**

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG  
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT  
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAAATTATGATAATTCT  
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTAGTCTCAATGAGCTCAAACCCACCCAC  
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA  
GGAGTCTATGTGGCATTTTGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG  
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA  
TTTTGCAATTTTGATGTCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA  
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTACCTTC  
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

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## FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG  
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCCGGCTGGGA  
CAAGAAGCCGCCGCCTGCTGCCCCGGGCCCGGGGAGGGGGCTGGGGCTGGGGCCGGAGGCGG  
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG  
TGTCTTGGGCACCTACCCGTGGGGCCCCGTAAGGCGCTACTATATAAGGCTGCCGGCCCCGAG  
CCGCCGCGCCGTGAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC  
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCCATCGCCGG  
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG  
ATCCTGGCCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC  
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCCGGCCCCC  
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGGACTGCGCGCGGGGC  
CAGAGCGCGCACAGTTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG  
CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT  
ACTCGGAGGAAGACTGTGCTTTGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA  
TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA  
CAGAGGCTTTCTTCCACTCTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG  
AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCGCCCTGGAGACCGACAGCATG  
GACCCATTTGGGCTTGTCACCGGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAACT  
GAGACCATGCCCGGCCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG  
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA  
GTTGTACATATTCAGAGTTTTCCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT  
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCTGGGCCCCCATTTCTGCTCCCTCGA  
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC  
TCACTTCCTTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTTTCTCATCACTTC  
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTTAATTTTCAGGAACAGGTGATCCACTCTGTA  
AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG  
ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCACCAG  
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAATTCCCC  
CTGAGGCCAGTTCTGTGATGGATGCTGTCTGAGAATAACTTGCTGTCCCGGTGTCACCTGC  
TTCCATCTCCAGCCCACCAGCCCTCTGCCCACCTCACATGCCTCCCCATGGATTGGGGCCT  
CCCAGGCCCCCCCACCTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAAAGAAAAGAT  
TTGAAGACCCCAAGTCTTGTCATAAATTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC  
CCTTTCCCCAGCACTTGGTTTTTCCAACATGATATTTATGAGTAATTTATTTTGATATGTACA  
TCTCTTATTTTCTTACATTATTTATGCCCCCAAATTATATTTATGTATGTAAGTGAGGTTTG  
TTTTGTATATTAAAATGGAGTTTGTGTTGT

## **FIGURE 22**

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDP IRLRHLYTSGPHGLSSCFLRI  
RADGVVDCARGQSAHSLLEIKAVLRRTVAIKGVH SVRYLCMGADGKMQG LLQYSEEDCAFEE  
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD  
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

### **Signal peptide:**

amino acids 1-22

### **Casein kinase II phosphorylation site.**

amino acids 78-82, 116-120, 190-194, 204-208

### **N-myristoylation site.**

amino acids 15-21, 54-60, 66-72, 201-207

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 48-59

## FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCTCGACCTCCTCA  
GAGCAGCCGGCTGCCGCCCCGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTCCTGCTG  
CTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCCAAA  
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA  
AGAAGACTGTTTTCTCCAGATTAGAGTGGAAGAACTGGGTCCGAGTGTCTCCTTTGTCTAC  
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG  
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG  
AGCAAGGCCAAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT  
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAAGTGTGGTAGAGCTACGATGTCAAGA  
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAGGATGGCATCCGTTTGCTAGAAA  
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACTGGAAGT  
CTGCAATTTAATACTGTTTCCAAACTGGACACTGGAGAATATTCTGTGAAGCCCGCAATTC  
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA  
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT  
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA  
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGAAGG  
CCGCGGCGGGCGGATCACGAGGTGAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC  
CATCTCTACTAAAATACAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC  
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC  
CACTGCAGTCCAGCCTGGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATA  
AATAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

CCGCGGCGGGCGGATCACGAGGTGAGGAGTTCTAGACCAGTCTGGCCAATATGGTGAAACCC

## **FIGURE 24**

MARRSRHRLLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE  
WKKLGRSVSFVYYQQTLOQDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED  
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST  
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNVSGYRRCPGKRMQVDDLNISGIIAAVVVVA  
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPVIPALWCAAAGGSRGQEF

### **Signal peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 130-144, 238-258

### **N-glycosylation site.**

amino acids 98-102, 187-191, 236-240, 277-281

### **Casein kinase II phosphorylation site.**

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

### **N-myristoylation site.**

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

### **Amidation site.**

amino acids 226-230

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[illegible]

AAAAACCAAGGAAACCTACTCCAAAATGAAC

## **FIGURE 26**

MKDMPLRIHVLLGLAITTLVQAVDKKVDPCRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT  
FPARLPANTQIILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE  
ENKLTTELPEKCLSELSNLQELYINHNLLSTISPGAFI GLHNLLRLHLNSNRLQMINSKWFDA  
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLEISFYDNRL  
IKVPHVALQKVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD  
LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSALYHGTIESLPNLKEISIHSPNIRC  
DCVIRWMNMNKTNI RFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICLPLIAPESFPSNLNV  
EAGSYVSFHCRTAEAPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC  
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFFV  
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE  
YEKNNTTTLMACLGGLLGIIGVICLISCLSPMNCDGGHSYVRNYLQKPTFALGELYPPLIN  
LWEAGKEKSTSLKVKATVIGLPTNMS

### **Signal sequence:**

amino acids 1-22

### **Transmembrane domain:**

amino acids 633-650

### **N-glycosylation site.**

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,  
608-612, 624-628, 625-629

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

### **Tyrosine kinase phosphorylation site.**

amino acids 570-579

### **N-myristoylation site.**

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,  
491-497, 492-498, 634-640, 702-708

### **Cell attachment sequence.**

amino acids 277-280

## **FIGURE 27**

CCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG  
CTGCAGCCTTTTGAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC  
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT  
GGTAGACCTGTGGTTAACCCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTTGTTCTTA  
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCCTCTGGG  
GGTTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCTCCTGA  
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAG  
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT  
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG  
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAACCCCTGGC  
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC  
AACGTGATCTGTAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC  
CAACGACGCTGACCTTTGTAACCTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA  
TGTTTGGCTGGTTCATATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG  
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA  
ACCTGATGATATTAGCACTGTGGTATTAGTGTCCAACTGACTGTCATTGAGAAAGAAAGAAA  
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA  
ACTTTGTATTTTCAGTTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA  
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT  
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT  
AATTTAAAAGCAAATAAAAGCTTAACCTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAAAAACA

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## **FIGURE 28**

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMCPCGCLCSSSGGLNVTCSNANLKEIPRDL  
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLSDNR  
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL  
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLSRQKK  
ADEPDDISTVV

### **Signal sequence:**

amino acids 1-33

### **Transmembrane domain:**

amino acids 205-220

### **N-glycosylation site.**

amino acids 47-51, 94-98

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 199-203

### **Casein kinase II phosphorylation site.**

amino acids 162-166, 175-179

### **N-myristoylation site.**

amino acids 37-43, 45-51, 110-116

## FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG  
GGCGTGAGGAGCATGCCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT  
GGGCTCAGTGCTGTCAGGCTCGGCCACGGGCTGCCCCGCTGCGAGTGCTCCGCCCAGG  
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG  
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCGCCAG  
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGGCG  
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC  
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAGAT  
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG  
ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG  
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACCTGCACGGCCT  
CATCGTCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC  
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC  
TGCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC  
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGTTTCTCAACCTCTCCTACAACCCCATCA  
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC  
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA  
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG  
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTGGCTCCTGTGGGTGTTCCGG  
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCAGTTTTGTCCA  
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCAACTACTTCACCTGCCGCCGCG  
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAGTTT  
GTGTGCCGGGCCGATGGCGACCCGCCGCCGCCATCCTCTGGCTCTCACCCCGAAAGCACCT  
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT  
ACGCCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCGGGCGGCAACGAC  
TCCATGCCCCGCCACCTGCATGTGCGCAGCTACTCGCCCGACTGGCCCCATCAGCCCAACAA  
GACCTTCGCTTTCATCTCCAACAGCCGGGCGAGGGAGAGGCCAACAGCACCCGCGCCACTG  
TGCTTTTCCCCTTCGACATCAAGACCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC  
CTGGGCGTCGTCCTCTTCTGCCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC  
AAAGCACAAACATCGAGATCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG  
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGGGGCGGGGGCAGGGACCCCCG  
GGCGGCCGGGCGAGGGGAAGGGGCCTGGTCGCCACCTGCTCACTCTCCAGTCTTCCCACCTC  
CTCCCTACCCTTCTACACACGTTCTCTTCTCCCTCCCGCCTCCGTCCCCTGCTGCCCCCG  
CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA  
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA  
ATAATTCAATAAAAAAGTTACGAACTTTCTCTGTAACCTGGGTTCATAAATTATGGATTTT  
TATGAAAACCTGAAATAATAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 30**

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF  
VAVPEGIPTETRLLDLGKNRIKTILNQDEFASFPHLEEELELNENIVSAVEPGAFNNLNLRTL  
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA  
FSGLSLEQLTLEKCNLTSLIPTALSHLHGLIVLRRLNLNINAI RDYSFKRLYRLKVLEISH  
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSM LHEL  
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTLEESVFHSGNLETLILDSNPLA  
CDCRLLWVFRRRWRLNFNRRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV  
FVDEGHTVQFVCRADGDP PAILWLSRPHKLVSAKSNGR LTVFPDGTLEVRYAQVQDNGTYL  
CIAANAGGND SMPAHLHVRSYSPDWPHQPNKTF AFISNQPGEGEANSTRATVPFPFDIKTLI  
IATTMGFISFLGVVLFCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 556-578

### **N-glycosylation site.**

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,  
492-496, 505-509, 526-530, 542-546

### **Casein kinase II phosphorylation site.**

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,  
607-611

### **Tyrosine kinase phosphorylation site.**

amino acids 590-598

### **N-myristoylation site.**

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,  
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 32-43

## FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTTCGGTCAAC  
ATCGTAGTCCACCCCCTCCCCATCCCCAGCCCCCGGGATTTCAGGCTCGCCAGCGCCCAGCC  
AGGGAGCCGGCCGGGAAGCGCGATGGGGGGCCCCAGCCGCCTCGCTCCTGCTCCTGCTCCTGC  
TGTTCGCCTGCTGCTGGGCGCCCGGCGGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG  
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCAAGTGCCAAGTGAAAGATCA  
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA  
GAGCCCTTCGAGATAATCGAATTCAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC  
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT  
GCGAACTGCCAAGTCCCTCGTCACTGTGTAGGAATTCCACAGAAGCCCATCATCACTGGTT  
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCAGTCTTCTGGGAGCAAG  
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT  
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC  
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC  
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC  
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC  
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT  
GCCCTGATCTTCCCTTTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG  
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCCAGTCCGGTGCCCT  
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCCTGCTG  
CTCATCATGCTCATCTTCCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA  
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG  
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTTCATCTAGAGGCGCCTGCCCACTTCCTGC  
GCCCCCAGGGGCCCTGTGGGGACTGCTGGGGCCGTCACCAACCCGGACTTGTAACAGAGCAA  
CCGCAGGGCCGCCCTCCCGCTTGCTCCCCAGCCCACCCACCCCCCTGTACAGAATGTCTGC  
TTTGGGTGCGTTTTTGTACTCGGTTTGGAATGGGGAGGGAGGAGGGCGGGGGAGGGGAGGG  
TTGCCCTCAGCCCTTTCGTGGCTTCTCTGCATTTGGGTTATTATTATTTTTGTAAACAATCC  
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAACA  
AACAAAAACA

## **FIGURE 32**

MGAPAASLLLLLLLLFACCWAPGGANLSQDDSQPWTSDET VVAGGTVVLKCQVKDHEDSSLQW  
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSSISINVALADEGEYTC SIFTMPVRTAKSLV  
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK  
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQR IEVLYTPTAMIRPDPPHPREGQ  
KLLHLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMG SYKA  
YYTLNVNDPSPVPSSSSSTYHAIIGGIVAFIVFLLLIIMLI FLGHYLI RHKGTYLT HEAKGSDD  
APDADTAIINAEGGQSGGDDKKEYFI

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 331-352

### **N-glycosylation site.**

amino acids 25-29, 290-294

### **Casein kinase II phosphorylation site.**

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

### **N-myristoylation site.**

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,  
306-310, 334-340, 360-364, 385-389, 386-390

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCTTTTCTTCTCCTTTCCTGG  
 CTTTCGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG  
 TTACTTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT  
 GCTGGAGACGTCTCTTTGTTTTGCCGCTGGAACGTTACAGGGGACGTTTGCAAAGAGAAGA  
 TCTGTTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA  
 AGTCTGCAGCGTTTCACTGCCCCGACTTCCCAGTTTTTACCATTTATTTCTGCATGGCAATTC  
 CCTCACTCGACTTTTCCCTAATGAGTTCGCTAACTTTTATAATGCGGTTAGTTTGCACATGG  
 AAAACAATGGCTTGCATGAAATCGTTCCGGGGGCTTTTCTGGGGCTGCAGCTGGTGAAAAGG  
 CTGCACATCAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA  
 TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG  
 ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCTACCTGCCAAC  
 GTGTTCCAGTATGTGCCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC  
 CTATGAGGAGGTCTTGAGCAAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCTTT  
 GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTTCCCAAGAATGCC  
 CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC  
 CACCGAACAGGACTTGTGTCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGGCGCCCCCTG  
 CCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG  
 GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT  
 CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAAACCCTTAGCTAACA  
 GTTTACCCTGCCCTGGGGGCTGCAGCTGCGACCACATCCCAGGGTCGGGTTTAAAGATGAAC  
 TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGCAGGA  
 GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA  
 ACCTCATTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAAG  
 AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA  
 GAAATTTCGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA  
 TCCTCCCGGGCACTTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAACAACCTG  
 CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGGGTCTCGCTCTCTAACTCAGCCTGCACAA  
 CAATTACTTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA  
 TAGACCTCCACGGAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA  
 GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT  
 TAGAAAGGATTTTATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT  
 CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTGGCGGAGACCGGGACGCACTCC  
 AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT  
 GTTTGTACCTCCGCCTTACCCTGGTGGGCATGCTCGTGTATATCCTGAGGAACCGAAAGC  
 GGTCCAAGAGACGAGATGCCAACTCCTCCGCGTCCGAGATTAATTCCTACAGACAGTCTGT  
 GACTCTTCTACTGGCACAATGGGCCTTACAACGCAGATGGGGCCACAGAGTGTATGACTG  
 TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGCG  
 ATACATCCTTCCCCACCGCAGGCACCCCGGGGGCTGGAGGGGCGTGTACCCAAATCCCCGCG  
 CCATCAGCCTGGATGGGCATAAGTAGATAAATAACTGTGAGCTCGCACAACCGAAAGGGCCT  
 GACCCCTTACTTAGCTCCCTCCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA  
 GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCAGCACGACCCTGCTGGAAG  
 AACTGACAGTGCCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC  
 ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTTTCCCCTGTGGATTAG  
 CCCCCTGATGGCTCCCTGTTGGCTACGCAGGGATGGGCAGTTGCACGAAGGCATGAATGTAT  
 TGTAATAAGTAACTTTGACTTCTGAC

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## **FIGURE 34**

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPT SQFYH  
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNNKIKSFRKQ  
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLEVLILNDNLISTLPANVFQYVPITHLDLRG  
NRLKTLPTYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ  
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTNGQEDHATPGSAPNGGK  
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSCDHIPGSGGLKMNCNNRNVSSLADLKP  
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLDDLRLWLYMDSNY  
LDTLSREKFAGLQNLLEYLNVEYNAIQILILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL  
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGPNWECSTIVPFKQWAERLGSEVLMSDLKC  
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL  
VPGLLLVFVTSFTTVVGMLVFILRNKRKRSDANSSASEINSLQTVCDSSYWHNGPYNADG  
AHRVYDCGSHSLSD

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 618-638

### **N-glycosylation site.**

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 122-126, 646-650

### **Casein kinase II phosphorylation site.**

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,  
608-612, 657-661, 666-670, 693-697

### **N-myristoylation site.**

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,  
354-360, 465-471, 493-499, 598-604, 603-609

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 337-348

## FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC  
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGTCGCGGCCTAAGGGAACTGTTGGC  
CGCTGGGCCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG  
AAGGGAGGGGGAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC  
AGCTCTGCGTCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGGCTCAG  
AGAATGAGGCGCGGTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCCGGGCGGGCGG  
CGGCGAACACCCCACTGCCGACCGTGCTGGCTGCTCGGCCTCGGGGGCCTGCTACAGCCTGC  
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC  
AGCACCGTGCGTGCAGGCGCGGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG  
GCCCCGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT  
GCACCTTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCCTCCGACCCCGGCGGTCTC  
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC  
GGTACTCCAGGCCACCGGTGGGGTGCAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC  
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTTGCGCCGCGCCCCGGG  
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG  
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGGACAGCTCCCGATCTCAGTTACTTGCA  
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC  
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG  
CTTTGCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA  
GTGGGGAAGGACAGCCGACCTTGGGGGGACCGGGGTGCCACCAGGCGCCCGCCGGCCACT  
GCAACCAGCCCCGTGCCGACAGAAACATGGCCAATCAGGGTGCACGAGAAGCTGGGAGAGAC  
ACCACTTGTCCCTGAACAAGACAATTCAGTAACATCTATTCTGAGATTCTTCGATGGGGAT  
CACAGAGCACGATGTCTACCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC  
CCATCAGGGAGCGTGATTTCAAAGTTAATTCTACGACTTCTCTGCCACTCCTCAGGCTTT  
CGACTCCTCCTCTGCCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGTTGGTGATCT  
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTCACGAAAGCCCCCTCTTCCCAGCCA  
AGGAAGGAGTCTATGGGCCCCGCGGGCCTGGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC  
CAGTTCTGCACATTGCACAAACAATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG  
CAGAGGGTGCTTGTGCTGGCGGAGTCCCCTCTTGGCTCTAGTGATGCATAGGGAAACAGGGGA  
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAACCTTAC  
TTGTGTAACGACAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCCTTTACTCCACTGAG  
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCTTTAGGA  
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTTCGGAGAA  
TTTGGAGAAGTGATTGAACTTTTCAAGACATTGGAAACAAATAGAACACAATATAATTTACA  
TTAAAAATAATTTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTTTCAAGGCTAGGAGTAT  
ATTGGTTCGAAATCCCAGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

## **FIGURE 36**

MRPAFALCLLWQALWPGPGGGGEHPTADRAGCSASGACYSLHHATMKRQAEEACILRGGALS  
TVRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE  
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA  
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCTADEIGARWDKLSGDVLCPCPG  
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPPATA  
TSPVPQRTWP I RVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP  
SGSVISKFNSTTSSATPQAFDSSSAVVFI FVSTAVVVLVILTM TVLGLVKLCFHESPSSQPR  
KESMGPPGLES DPEPAALGSSSAHCTNNGVKVGDCDLRDR AEGALLAESPLGSSDA

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 399-418

### **N-glycosylation site.**

amino acids 189-193, 381-385

### **Glycosaminoglycan attachment site.**

amino acids 289-293

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 98-102, 434-438

### **Casein kinase II phosphorylation site.**

amino acids 275-279, 288-292, 342-346, 445-449

### **N-myristoylation site.**

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,  
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,  
477-483

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 262-274

## FIGURE 37

CGGACGCGTGCGGATTTCAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG  
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCTCCGCCCTGCCGGCCGCGTATC  
CCCCGGCTACCTGGGCCGCCCGCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA  
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGGCGGTGTGAGCGCGGTGGGTGCGGA  
GGGGCGTGTGTGCCGGCGCGCGCGCGCGTGGGGTGCAAACCCGAGCGTCTACGCTGCCATGA  
GGGGCGCGAACGCCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG  
CAGCAGTCCCCAGAGAGACCTGTTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT  
TATTGGCAGTGAAGGTTTTCTGGAGTGTACCCTCCAAATAGCAAATGTACTTGGAAAATCA  
CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTCATAGACCTCGAGAGTGACAAC  
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCCG  
CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA  
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA  
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC  
CCCCAACTGGCCAGACCGGGATTACCCTGCAGGAGTCACTTGTGTGTGGCACATTGTAGCCC  
CAAAGAATCAGCTTATAGAATTAAAGTTTTGAGAAGTTTTGATGTGGAGCGAGATAACTACTGC  
CGATATGATTATGTGGCTGTGTTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA  
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTAGT  
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA  
AACTGCCTACAACACAGAACAGCCTGTCACCACCACATTCCCTGTAACCACGGGTTTTAA  
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT  
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAAACCATCACTCGCGATGGGAGTTTG  
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTGAGCAGGCGGG  
CAAGAACATGAGTGCCAGGCTGACTGTCGTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC  
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC  
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG  
TTAAACAGTGAAGTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT  
TCTCAGTAGAAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG  
GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT  
TGCCTGCTGTCAGAGGAGCAGCTATCTGATTGGAAACCTGCCGACTTAGTGCGGTGATAGGA  
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTTATACATCTCTGTAAAAGGAT  
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTTATAGT  
GTTATTTGTTTCACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTA  
AATCAATGCTTAATAAAATATTTTAAAGGAAAAAAAAAAAAA

## **FIGURE 38**

MRGANAWAPLCLLLAAATQLSRQQSPERPVFCTCGGILTGESGFIGSEGFPGVYPPNSKCTWK  
ITVPEGKVVLNFRFIDLES DNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV  
QMISDANTAGNGFMAMFSAAEPNERGDQYCGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV  
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSEARNELLI  
QFLSDLSLTADGFIGHYIFRPKKLP TTTTEQPVT TTFPVT TGLKPTVALCQQKCRRTGTLEGN  
YCSSDFVLAGTVITTTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR  
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

### **Signal sequence:**

amino acids 1-23

### **N-glycosylation site.**

amino acids 355-359

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 142-146, 274-278

### **Tyrosine kinase phosphorylation site.**

amino acids 199-208

### **N-myristoylation site.**

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,  
305-311, 309-315, 320-326, 330-336

### **Cell attachment sequence.**

amino acids 149-152

## **FIGURE 39**

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGGGCTGGGGCGGTGCTTCTT  
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG  
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG  
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG  
CCGGGGACTGGTTGACAGCTTTAAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG  
GTGGAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG  
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT  
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTCACAAGCAGCAGGAGGCCCCGGACCTCTTCC  
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGAGGCACCTTCGGGGCCCTCCTGC  
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG  
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC  
AGTGTGTCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT  
TTTGGCCCCCTGTGCCCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG  
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT  
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG  
GCCTGCCTAGGCTGCATGGGGGCAGGGCCAGGTGCTGTGAAGAAGTGTAGCCCTGGCTATCA  
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA  
ACAAGCAGTGTGAAAACACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG  
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC  
AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA  
CGCTGGCTGCTAAGGGCGACTTGGTGTTACCGCCATCTTCATTGGGGCTGTGGCGGCCATG  
ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA  
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGCTGCCC  
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTG  
CCTTACAGAGCAGCCCAGGTACCCAGGCCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC  
CCTGAAGGTGATACCATGAGCTCTTCACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA  
ATTTCAAAAGTTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG  
GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT  
TCTGTGTTACACATCCCCACACCCATTGCCACTTATTTATTCATCTCAGGAAATAAAGA  
AAGGTCTTGAAAGTTAAAAA

## **FIGURE 40**

MAPWPPKGLVPAVLWGLSLFLNLPGPPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER  
TIRDNFGGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ  
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCQAG  
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPESNCLQCKKGWALHHLKCVDIDE  
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE  
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDLVVLQQMFFG  
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

### **Signal sequence:**

amino acids 1-29

### **Transmembrane domain:**

amino acids 372-395

### **N-glycosylation site.**

amino acids 79-83, 205-209

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 290-294

### **Casein kinase II phosphorylation site.**

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

### **N-myristoylation site.**

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,  
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,  
326-332, 372-378, 395-401

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 321-333

### **EGF-like domain cysteine pattern signature.**

amino acids 181-193

## FIGURE 41

TCGAGACCCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA  
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCCCTGGCCAGCCCCGGG  
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT  
GCCCCACCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT  
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTTACGCCAGAGC  
TTCCGAGAGGTGGCCGGCAGGTTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG  
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG  
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCCGGGCC  
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA  
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA  
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG  
GAGCATCTGGGCCCCGCTGGCGTCCGGCGCCCCACAAGCTGGTCCGCTTTGCCTCGCAGGGGGC  
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCCTGGACCTTGGGGACTATGGAG  
CTCAGGGCGACTGTGACCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG  
ATGTACATTGACCTGCAGGGGATGAAGTGGGCGGAGAACTGGGTGCTGGAGCCCCCGGGCTT  
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTTCAAGTGGC  
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC  
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA  
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATTAGGCGCCTAGTG  
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTTCGAGGGTACCAGGAGAGCTG  
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT  
CCTCTGACAAGTTACCTCACCTAATTTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA  
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCACTGCACTATATTCTAAGCACTTACAT  
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTTACTTGTCTGTGTCAC  
TGGATCTGGGCTAAAGTCTCCACCACCACTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT  
TGTGCATCCCCAATCCAGATAATAAAGACTTTGTAAAACATGAATAAAACACATTTTATTCT  
AAAA

## **FIGURE 42**

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV  
ALLQRSHGDRSRGKRFSQSFRVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRRLFQEP  
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF  
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ  
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWPF  
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKSCASDGALVPRRLQP

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 158-162

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 76-80

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

### **N-myristoylation site.**

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

### **Amidation site.**

amino acids 74-78

### **TGF-beta family signature.**

amino acids 282-298

## FIGURE 43

GTCTGTTCCCAGGAGTCCTTCGGCGGCTGTTGTGTCAGTGGCCTGATCGCGATGGGGACAAA  
GGCGCAAGTCGAGAGGAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG  
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT  
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGGAAGTTTGACCA  
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG  
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC  
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT  
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG  
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT  
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCCT  
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCCTGTGAGCCTCTGATACTGGAGAATACA  
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT  
GTGGAGCGGAATGTGGGGGTGTCGTGGCAGCCGTCTTGTAACCCTGATTCTCCTGGGAAT  
CTTGGTTTTTTGGCATCTGGTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA  
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG  
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCTTACT  
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC  
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTCAGCTATGTGCCCC  
ATCCTCCTTCATGCCCTCCCTCCCTTTTCTTACCCTGCTGAGTGGCCTGGAACCTGTTTAA  
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC  
TTCTAAGTAGACAGCAAAAATGGCGGGGGTTCGAGGAATCTGCACTCAACTGCCCACCTGGC  
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTTCCTTGTGTACTGAC  
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG  
TGATGACACTGGGGTCCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG  
CCACTGGGATCCCTCTGCCCTGTCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT  
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG  
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG  
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTCGGGAGTTTCGGGATCAGCCTGACCA  
ACATGGAGAAACCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC  
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSLAYSGFSSPRVEW  
KFDQGDTTTRLVCYNNKITASYEDRVTFLLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV  
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS  
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI  
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

### **Signal sequence:**

amino acids 1-27

### **Transmembrane domain:**

amino acids 238-255

### **N-glycosylation site.**

amino acids 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 270-274

### **Casein kinase II phosphorylation site.**

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,  
193-197, 203-207, 287-291

### **N-myristoylation site.**

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

## FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA  
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT  
GGAGGCCGCCGCGAGCCCGCTTTCCACCCCGACCTCTGCCCAGGCCGCGAGGCCCCAGCTCAG  
GCTCGTGGCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTTATGCGTGCCCCCTCACCTGG  
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGACAGGATTGAGCC  
ATGTACCCAGAAAGGGCAATGCCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCA  
GTGACTGCTCTGGGGGAAGTACAAAGAACTGCGCAACTGCAGCCGCCTGGCCTGCCTAGCA  
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA  
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG  
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC  
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCTCTGTGCGGAATGCCACATCCTC  
CTCTGCCGGAGACCAGTCTGGAAGCCCCAACTGCCTATGGGGTTATTGCAGCTGCTGCGGTGC  
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC  
CTCCGCCCCTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTCAGAACAGAAGAC  
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA  
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT  
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC  
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG  
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG  
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

## **FIGURE 46**

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSQAAGPSSGSCPPTKFQCR  
TSGLCVPLTWRCRDLDCSDGSDEEEECRIEPCQTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL  
RNC SRLACLAGELRCTLSDDCIPLTWRC DGHDPDCPDSSDELGCGTNEILPEGDATTMGPPVT  
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL  
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

### **Signal sequence:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 230-246

### **N-glycosylation site.**

amino acids 126-130, 195-199, 213-217

### **Casein kinase II phosphorylation site.**

amino acids 84-88, 140-144, 161-165, 218-222

### **N-myristoylation site.**

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,  
224-230, 230-236, 263-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 44-55

### **Leucine zipper pattern.**

amino acids 17-39

## **FIGURE 47**

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGGCACAGATGCGG  
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA  
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG  
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG  
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT  
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG  
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG  
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAATGGAACCCTAGGCTGGATCCCAAGTGA  
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTATA  
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTTCATGAAGGATTCAAGATCCGG  
TACCCCGACCTACACAATATGGTTTCATTATGTGCGCATGATGGAACGTGGAATAATCTGCC  
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC  
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTTCCCGGATTTAAACTT  
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG  
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTTCGTCT  
GCCACCCGCGGCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTTACTGCGATCCT  
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC  
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCCAGCACCCATGAGACCCTCCTGA  
CCACGTGGAAGATTGTGGCGTTACGGCAACCAAGTGTGCTGCTGGTGTCTGCTGCTCGTCATC  
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCTCCCCGGAG  
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCCCTATG  
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG  
GGCTGCCCCCTTACCCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGGACACGGA  
CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA  
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATA  
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCCCTGGGT  
GTTGTTCCCTAAGAACTTGATTGATTAAAAAATTTCCCAAAGTGTCTGAAGTGTCTCTTCAA  
ATACATGTTGATCTGTGGAGTTGATTCCTTTCTTCTCTTGGTTTTAGACAAATGTAAACAA  
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC  
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAAGNAAAAA

## **FIGURE 48**

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI  
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI  
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS  
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP  
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT  
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFAHFPPRGPPRSSSSDPDFVVVD  
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGD TDTGPGESETCDS  
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVFLRN

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 325-344

### **N-glycosylation site.**

amino acids 104-108, 134-138, 192-196

### **Casein kinase II phosphorylation site.**

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,  
364-368, 380-384, 467-471, 468-472

### **N-myristoylation site.**

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,  
478-484

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 394-405

## FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGA  
TGCTGCTGCCGCGGTTGCAGTTGTGCGCACGCCTCTGCCCCGCCAGCCCGCTCCACCGCCGT  
AGCGCCCAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCGCGCTACAGG  
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC  
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTTA  
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT  
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA  
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGA CTCTGGATTGGGCTCAGGAGGCGTGA  
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT  
CACAATTTAGGAACTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATG  
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCCCTACATGTTCCAGTGGAATGATGA  
CCGGTGCAACATGAAGAACAATTTCA TTTGCAAATATTCTGATGAGAAACCAGCAGTTCCTT  
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG  
GAAGAAGATGCCAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT  
CCTAATCCCCAGCATTCCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTT  
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC  
TGGCCCTCTCCTCACCAGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA  
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCA TTTCCGAGTGTGTT  
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA  
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGA  
GTTCTCCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG  
GTTATTAGGACATATAAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC  
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT  
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTTGGCTGTATCCTTTAT  
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCCAGGTCTGGCACATAGTA  
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG  
GCAGTGATAAAGATGGGCTGTGGAGCTTGGA AAACACCTCTGTTTTCTTGCTCTATACAG  
CAGCACATATTATCATAACAGACAGAAAATCCAGAATCTTTTCAAAGCCCACATATGGTAGCACAG  
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAAATAAAGA  
GCAGGAAAAAAAAA

## **FIGURE 50**

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL  
NFEEAKEACRRDGGQLVSI ESEDEQK LIEKF IENLLPSDGD FWIGLRRREEKQSNSTACQDL  
YAWTDGSI SQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY  
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLLLV  
VTTVVCWWVICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL  
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKES  
GWVENEIYGY

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 117-121, 312-316

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 296-300

### **Casein kinase II phosphorylation site.**

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,  
299-303, 306-310, 323-327

### **N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

## FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC  
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT  
GTTTGCCCTCCTGCAGCCTCAACCCGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT  
GTTCAGCATGCGCTTGTGGACCCCAGTGGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC  
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC  
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC  
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCCCAACTC  
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT  
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT  
GCAGCAAATGTTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC  
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTTCGTTCCACTAACATTTTTTCGGAATCTG  
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTCAGAAAGAAGGACCCATCATCAT  
CCCACTGATGAAGCAGATTGAGAAGTCTTGTATCCCAACTACCAAAGCTGCTGGAGCCTGA  
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG  
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGAAGTCTTTCATCCTCCT  
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCCATGCTGAAGAGATTTG  
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGTACATACTGCCCAAGGAAGACAGG  
GAAAGTCTTCAGATGGCAGTAGGCCCATTCCTCCACATCCTAGAGAGCAACCTGCTGAAAGC  
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG  
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGGACCACAAATGGCCACCGTTTGCT  
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA  
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCCGCTGGACATGT  
TCTTGAATGCCATGTCAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA  
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT  
TTAAAATAAAGTGCCTTTATACAATG

[illegible]

Signal sequence:

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

**Tyrosine kinase phosphorylation site.**

N-myristoylation site.

Amidation site.

Leucine zipper pattern.

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

## FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT  
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT  
GCCATTTGCACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGCGGCTGGTGGGGGGCCT  
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG  
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC  
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCCTCATCCA  
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG  
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCAGAGAGCTCTTTCTCCCCA  
GTCCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAGTGAA  
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG  
TGTGCCCGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC  
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTTCA  
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTGC  
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG  
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA  
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA  
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTCTGCTCAGGGGAGGAG  
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA  
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA  
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT  
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG  
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA  
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT  
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA  
CACCATTTGTCCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA  
TTCTAGAGGAACGGAATTTTAAGGATAAAATTTTCTGAATTGGTTATGGGGTTTCTGAAATTG  
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTTATTTACAATAATAAGATAGCAC  
TATGTGTTCAAA

## **FIGURE 54**

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC  
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC  
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRLGCGRAVL  
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG  
GDNLCSGRLEVLHKGWVGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL  
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

### **Signal sequence:**

amino acids 1-15

### **Casein kinase II phosphorylation site.**

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,  
267-271, 294-298, 316-320, 336-340

### **N-myristoylation site.**

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,  
180-186, 263-269, 286-292

### **Amidation site.**

amino acids 196-200

### **Speract receptor repeated domain signature.**

amino acids 29-67, 249-287

[illegible]

ACTGCACACTCGGTTCTATCGAATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG  
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCCTGCTGTTTCGGCTGCCTGGG  
CGTCTTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCTACCTGCGGAATGCTG  
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT  
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA  
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC  
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC  
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA  
TGTGGACAAGAGGGTCATGGAGACAAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC  
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTGCGCCATCAGCAGCATCCAGGGCAAG  
ATGAGCATTCCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA  
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA  
TCCACACCAACCTCTCTGTAAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC  
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCCAGGATGTTCTTGCTGCTGTGGG  
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGCTGTTTATCTTCGAA  
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC  
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTG  
TACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTTGTCTCACAAGTGGG  
AAAGACTGAAGAAACACATCTCGTGACAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA  
AGCTTCTTCCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACT  
AAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG  
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTAC

## **FIGURE 56**

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA  
KLVLGCRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEILQCFGYVDIL  
VNNAGISYRGTIMDTTVDDVKRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGMKSI  
PFRSAYAASKHATQAFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT  
AQGRSPVEVAQDVLAAVGKKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

### **Signal sequence:**

amino acids 1-21

### **Transmembrane domain:**

amino acids 104-120, 278-292

### **N-glycosylation site.**

amino acids 228-232

### **Glycosaminoglycan attachment site.**

amino acids 47-51

### **Casein kinase II phosphorylation site.**

amino acids 135-139, 139-143, 253-257

### **Tyrosine kinase phosphorylation site.**

amino acids 145-153, 146-153

### **N-myristoylation site.**

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

### **Amidation site.**

amino acids 265-269

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 6-17

## **FIGURE 57**

CCCACGCGTCCGCTGGTGTTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA  
AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC  
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA  
GAGGAGAAAATCAGTCACCGGCGAAATCGTGCTGATTACAGGAGCTGGGCATGGAATTGGGA  
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTTCTCTGGGATATAAATAAG  
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTACATCCTTTGT  
GGTAGACTGCAGCAACCGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG  
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA  
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA  
GGCATTTCCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG  
CTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA  
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG  
TCTGTGTCCTAATTTTCGTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA  
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG  
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT  
CCTGGCAGTTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA  
AAGCGCAATAAAGCACCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCATCTA  
ATAGTGCCAGAATTTTAATGTTTGAACCTTCTGTTTTTTCTAATTATCCCATTTCTTCAATA  
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT  
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA  
CCAAAATGACTTTATTAAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA  
AATTTGTACCATAACCGTTTTATTTAACATATATTTTTATTGATTGCACTTAAATTTTGT  
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA  
TGAAGGACTATATCTAGTGGTATTTACAAATGAATATCATGAACTCTCAATGGGTAGGTTTC  
ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT  
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG  
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA  
AA  
AA

[illegible]

**Signal sequence:**

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

## FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGGCTC  
AGGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG  
TTTCGCTGGTCCTGTTGATGCCTGGCCCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT  
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC  
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCAGGACTGAACATGA  
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTC  
TTCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG  
AGGTTTCATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGA  
CCTTGCGTGACAGAGACTTCCCCTGACCACAACGCTCTCCATGCTTTACATTGACAATCCA  
GTGGGCACAGGCTTCAGTTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT  
AGCACGGGATTATACAGTGCCTAATTGAGTTTTTCCAGATATTTCTGAATATAAAAAATA  
ATGACTTTTTATGTCACTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC  
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA  
TGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCT  
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC  
AGGAAGCAGAACTGGTTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC  
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT  
GCACGGAACCTGAGGATCAGCTTTTACTATGTGAAATTTTTGTCCTCCAGAGGTGAGACAA  
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACATAGTTGAAAAGTACTTGCGAGA  
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA  
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC  
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAAGTTTGGAAGATCTTTAA  
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC  
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA  
TTCATTTATGGAAAAGGATGGGATCCTTATGTTGGATTAATACTACCTTCCCAAAAGAGAACAT  
CAGAGGTTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA  
TTATCTTTTCATATCTGCAAGATTTTTTTTCATCAATAAAAAATTATCCTTGAAAACAAGTGAGC  
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA  
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA  
AATTTTAGGGTCTTGAATAGGAAGTTTTAATTTCTTCTAAGAGTAAGTGAAAAGTGCAGTTG  
TAACAAACAAAGCTGTAACATCTTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT  
GTTTGGAATATTATTGGATAAGAATAGCTCAATTATCCCAAATAAATGGATGAAGCTATAA  
TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAATTCTTTGAAATA  
AAAATATTATATATAAAAGTAAAAAAAAAA

## **FIGURE 60**

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL  
VGPFPGGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH  
GPYVVTSNMTLRDRDFPWTTTSLMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF  
FQIFPEYKNNDFYVTGESYAGKYVPAIAHSLNPVREVKINLNGIAIGDGYSDPESIIGG  
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVGTG  
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT  
EIMNNYKVLINYGQLDIIVAAALTERSLMGMDWKGSGQEYKKAEEKVWKIFKSDSEVAGYIRQ  
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 81-85, 132-136, 307-311, 346-350

### **Casein kinase II phosphorylation site.**

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,  
353-357, 424-428

### **Tyrosine kinase phosphorylation site.**

amino acids 423-432

### **N-myristoylation site.**

amino acids 22-28, 110-116, 156-162, 232-238

### **Serine carboxypeptidases, serine active site.**

amino acids 200-208

### **Crystallins beta and gamma 'Greek key' motif signature.**

amino acids 375-391

## FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT  
TTTTCCCTTTCCTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT  
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTTG  
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG  
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC  
CTGGGGGAGGGCCTGCCTAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT  
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCTAATATCAAATTGACTGGCTGGG  
TGAACCTTCAACAGCCTTTTAACTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA  
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA  
GACCAAAATAGATAACAGGATTCCCTGAACATTCTTAAGAGGGAGAAAGTATGTTAAAAATA  
GAAAAACCAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCTGGGTG  
AGGCCAGCCTCTTTGCTCCTCCCGGAAATTATTTTGGTCTGACCACTCTGCCTTGTGTTTT  
GCAGAAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT  
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG  
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCCAGCAGCCGGC  
ATGCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT  
CCACCAAGGGACGGGGGCCGTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA  
ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG  
CCCCCTCATCGTGACGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCT  
CATCATTTGACTACTCTGAGAACCCTGCTGGCCTGTGGGAGCCTCTACCAGGGGTCTGCA  
AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC  
CTGTCCAGTGTCACAAGACGGGCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA  
TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTCCA  
GCCGGAAGCTGCCCCGAGACCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT  
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCCTGGCCCTGGTCTCCCACTTTGACAT  
CTTCTACATCTACGGCTTTGCTAGTGGGGCTTTTGTCTACTTTCTCACTGTCCAGCCCGAGA  
CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG  
CTCTGCAAGGATGACCCCAAGTTCCACTCATACTGTCCCTGCCCTTCGGCTGCACCCGGGC  
CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC  
AGGCCTTCAATATCACAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG  
CAGTATCACCAACCCGCCGATGACTCTGCCCTGTGTGCCCTTCCCTATCCGGGCCATCAACTT  
GCAGATCAAGGAGCGCCTGCAGTCTGTCTACCAGGGCGAGGGCAACCTGGAGCTCAACTGGC  
TGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA  
CTGGACATCAACCAGCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCCTGTACACCAC  
CAGCAGGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAACGGCTACAGCGTGGTTTTTG  
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC  
ATTACCTCCTCAGCAAAGAGTCCCTCTTGGAAAGGTAGCTATTGGTGGAGATTTAACTATAG  
GCAACTTTATTTTCTTGGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGGTAAATTTTGTG  
ACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA  
TTTCAATATTTCCCAAACCTTAAAGAAAAACTTTAAGAAGGTACATCTGCAAAAGCAAA

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTTGGCTACAACAT

## **FIGURE 62**

MGTLGQASLFAPPGNYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP  
RALEVDSRSVVLVSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV  
YKLTGNLTIQVAHKTGPEEDNKSRYPPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL  
YQGVCKLLRLDDLFIIVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY  
FPTLSSRKLPRDPRESSAMLDYELHSDVSSLIKIPSDTLALVSHFDIFYIYGFASSGGFVYFL  
TVQPETPEGVAINSAAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP  
GDSLAQAFNITSQDDVLFALFSGKQKQYHHPPDDSAFCFPIRAINLQIKERLQSCYQEGN  
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG  
YSVVFGTKSGKLLKVRVYEFRCNAIHLSSKESLLEGSYWWRFNRYRQLYFLGEQR

### **Signal sequence:**

amino acids 1-32

### **Transmembrane domain:**

amino acids 71-87

### **N-glycosylation site.**

amino acids 130-134, 145-149, 217-221, 381-385

### **Casein kinase II phosphorylation site.**

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,  
384-388, 471-475, 481-485, 530-534

### **N-myristoylation site.**

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

## FIGURE 63

AGGCTCCCGCGCGCGCTGAGTGC GGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAACACGCGATGACCA  
CGTGGAGCCTCCGGCGGAGGCCGGCCCCGCACGCTGGGACTCCTGCTGCTGGTCTGCTTTGGGCTTCTTGGTGCTCC  
GCAGGCTGGACTGGAGCACCCCTGGTCCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA  
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTGGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT  
GGAGGGACCGCCTGCTGAAGATGAAGGCCCTGTGGCTTGAACACCCCTCACCACCTATGTTCCGTGGAACCTGCATG  
AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCCTTCGTCCTGATGGCCGCAGAGATCG  
GGCTGTGGGTGATTCTGCGTCCAGGCCCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGCCAGCTGGCTAC  
TCCAAGACCCTGGCATGAGGCTGAGGACAACCTTACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACC  
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG  
GTTCCCTATAATAAAGAACCCCGCATACATGCCCCACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACCTGC  
TCCTGACTTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGGCCACCATCAACTTGCAGT  
CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT  
ACTGGACGGGGTGGTTTGGACTCGTGGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT  
CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCACGGAGGCACCAACTTTGGCTTCATGAATG  
GAGCCATGCACTTCCATGACTACAAGTCAGATGTCACCAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG  
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG  
ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC  
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCCT  
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG  
TGTTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT  
ACACCGTGCTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG  
GCTTAATTGGAAATCTCTATCTGAATGATTACCCCCGAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA  
GCTTCTTTTTCAGAGGTTTCGGCCTGGACAAATGGNGTTCCCTCCAGAAAACACCCACATTACCTGCTTTCTTCTTGG  
GTAGCTTGTCCATCAGCTCCACGCCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA  
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTTGGACCCCAAGACGCTTTACCTCCAGGTCCCTGGTTGA  
GCAGCGGAATCAACCAGGTCATCGTTTTTGGAGAGACGATGGCGGGCCCTGCATTACAGTTCACGGAAACCCCCC  
ACCTGGGCAGGAACAGTACATTAAAGTGAAGCGGTGGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCTC  
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG  
ACTGGGGGCTACAGTCTGCCCCGTGTCTCAGCTCAAAACCTAAGCCTGCAGGGAAAGGTGGGATGGCTCTGGGCC  
TGGCTTTGTGATGATGGCTTTTCTACAGCCCTGCTCTTGTGCGGAGGCTGTGCGGCTGTCTCTAGGGTGGGAGC  
AGCTAATCAGATCGCCCAGCCTTTGGCCCTCAGAAAAAGTGCTGAAAACGTGCCCTTGCACCGGACGTCACAGCCC  
TGCGAGCATCTGCTGGACTCAGGCGTGCTCTTTGCTGGTTCTTGGGAGGCTTGGCCACATCCCTCATGGCCCCAT  
TTTATCCCCGAAATCCTGGGTGTGTACCAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT  
CTTCCTTCAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAAACATGTGACTTCCCCCTT  
TCCCTTCCCACTCGCTGCTTCCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCCTCACCTGCGTCTTCC  
CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCA  
CATCCAGGGAGGAGGACAGAAGGCCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCC  
AGGGAGGAGGACAGAAGGCCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGA  
GGAGGACAGAAGGCCCAGCTCACATGTGAGTCTTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGG  
ACAGAAGGCCCAGCTCAGTGGCCCCCGCTCCCCACCCCCACGCCCCGAACAGCAGGGGCAGAGCAGCCCTCCTTC  
GAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCTCTGA  
GTTGCAGTAAAGCTATAACCTTGAATCACAA

## **FIGURE 64**

MTTWSLRRRPARLGLLLLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW  
IFGGSIHVFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFDFSGNLDLEAFVLMA  
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVDLYFDHLMSRVVPLQ  
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLTSDNKDGLSKGIVQGVLAT  
INLQSTHELQLLTTFLFNVQGTQPKVMMEYWTGWFDSWGPHNILDSSSEVLKTVSAIVDAGS  
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP  
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYE  
TSITSSGILSGHVHDRGQVFVNTVSIQFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN  
IDDQRKGLIGNLYLNDSPKFNRIYSLDMKKSFFQRFGLDKWXSLETPETPLPAFFLGSLGIS  
STPCDTFLKLEGWEKGVVFINQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA  
LQFTETPHLGRNQYIK

### **Signal sequence:**

amino acids 1-27

### **Casein kinase II phosphorylation site.**

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

### **N-myristoylation site.**

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,  
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

## FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC  
CTGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG  
GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC  
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC  
AAGAAGCTGTCCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCA  
GGCAGACACTCGGTTCGTTCTAGTGGATAGGGGTTCATGACCGGTTTCTCCTAGACGGGGCCC  
CGTTCCGCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC  
CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACCTA  
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGA  
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG  
TGGGAGATGGGGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC  
AGATCCAGACTTCCTTGCCGAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC  
CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTGAGGTGGAGAATGAATATGGTAGC  
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGGCTCTTCCGTGCACTGCTAGG  
AGAAAAGATCTTGCTCTTACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG  
GACTCTATACCACTGTAGATTTTGGCCCAGCTGACAACATGACCAAAATCTTTACCCTGCTT  
CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA  
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAACCAAAGGACTAGAGAACATGC  
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG  
AATGGTGGCGATAAGAAGGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC  
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGT  
TCCAGGAAGTTCCTTTGGGACCTTTACCTCCCCCGAGCCCCAAGATGATGCTTGGACCTGTG  
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCCAT  
TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC  
GAACCTATATGACCCATACCATTTTTTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC  
CATGACCGTGCCTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTGGAGCGAAATATGAG  
AGACAAACTATTTTTGACGGGGAAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG  
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG  
GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG  
GTGGTTTCCCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT  
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG  
ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCGGTAAGTGGACAAAGCAGGGGCC  
ACAACAGACCCCTCTACGTGCCAAGATTCCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA  
CATTGCTGGAAC TAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTTGGATAAGCCTATC  
CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCCTTTTCTAGCTGATACACTGAG  
TGCCTCTGAACCAATGGAGTTAAGTGGGCAC TGAAGGTAGGCCGGGCATGGTGGCTCATGC  
CTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA  
CCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGGCGTG  
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC  
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA  
GACACTCCATCTCAAAAAAAAAAAAA

## **FIGURE 66**

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL  
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI  
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE  
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVD FGPADNMTKIF  
TLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMVMFHGGTNF  
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPPSPKMML  
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN  
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNS SDFKGLLKP  
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGD TFLYL  
PGWTKGQVWINGFNLGRYWTKQGPQOTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD  
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

### **Signal sequence:**

amino acids 1-27

### **N-glycosylation site.**

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 4-8

### **Casein kinase II phosphorylation site.**

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,  
603-607, 644-648

### **Tyrosine kinase phosphorylation site.**

amino acids 191-198

### **N-myristoylation site.**

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,  
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

## **FIGURE 67**

GCTTTGAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC  
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT  
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT  
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCCAGATGTCAAAAACGATTTT  
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT  
CTTGTGAGAAGTTAGTGAAAATAAACTTAGGGAAATTAGTTTGAACCATGAGTGGACATTTG  
AAAAACTCAGGCAGCACATTTTACGCAACGCCCAGGACAAGCAGGAGTTGCATCTGTTTCATG  
CTGTCGGGGGTGCCCGATGCTGTCTTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC  
AATTCAGAAGCTAAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC  
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA  
TGCCTTCACGTGAAGTTCAGTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA  
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAACAATAAGATGATAGGACTTG  
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT  
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTCATAATGACGGCAC  
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA  
ACTGTGAGCTAGAGAGAATCCACATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT  
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAACGACT  
GACTTGTTTAAAATTTATGGCATAACAAAATTGTTACTATTCCCTCCCTCTATTACCCATGTCA  
AAAACCTTGAGTCACTTTATTTCTCTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT  
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA  
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTCTGC  
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAACTGCATCACC  
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG  
CTTGGACCGCCTGCCAGCCAGCTGGGCCAGTGTCGGATGCTCAAGAAAAGCGGGCTTGTTG  
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA  
AATATTCCTTTTGCAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC  
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG  
ATACATCTTTTAAAATAAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT  
GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTTCCAAATCATTTTTTTTTTTCTTTTGGGG  
AAAGGGAAGGAAAAATTATAATCACTAATCTTGGTTCTTTTTAAATTGTTTGTAACTTGAT  
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT  
TTCTTACTAAAAA

## **FIGURE 68**

MAYMLKKLLISYISIIICVYGFI~~C~~LYTLF~~W~~LFRIP~~L~~KEYSFEK~~V~~REESSFS~~D~~IPDVKN~~D~~FAFL  
LHMVDQYDQLYSKRFGVFLSEVSENKLREISLNHEWTFEKL~~R~~QHISR~~N~~AQDKQELHLF~~M~~LSG  
VPDAVFDLTDL~~D~~VLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL~~R~~DHL~~R~~CLH  
VKFTDVAEIPAWVYLLK~~N~~LRELYLIGNLSEN~~N~~KMIGLES~~L~~REL~~R~~H~~L~~KILHV~~K~~SNLTKVPSN  
ITDVAPHLTKLVIHNDG~~T~~KLLVLNSLKKMMNVAE~~L~~ELQNC~~E~~L~~R~~IPHAIFSL~~S~~NLQELDLKS  
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES~~L~~YFSNNKLES~~L~~PVAVFSLQ  
KL~~R~~CLDVSYNNISMIP~~I~~EIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLN~~L~~GQNCITS~~L~~P  
EKVGQLSQLTQLELKG~~N~~CLDRLPAQLGQCRMLKKSGLVVEDHLFD~~T~~LPLEVKEALN~~Q~~DINIP  
FANGI

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 241-245, 248-252, 383-387

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 326-330

### **Casein kinase II phosphorylation site.**

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

### **Tyrosine kinase phosphorylation site.**

amino acids 349-355, 375-381

### **N-myristoylation site.**

amino acids 78-84, 124-130, 212-218, 392-398

[illegible]

CCACACGCGTCCGGCCCTTCTCTCTGGACTTTTGCATTTCCATTCCCTTTTCATTGACAAACTGACTTTTTTTTTATTTCCT  
TTTTTTTCCATCTCTGGGGCCAGCTTGGGGATCCTAGGGCCGCCCTGGGAAGACATTTGTGTTTTACACACATAAGGAT  
CTGTGTTTGGGGTTCCTTCTTCCCTCCCCTGACATTGGGCATTGCTTAGTGGTTGTGTGGGGAGGGAGACAGCTGG  
GCTCAGTGTGCTTGGCACTTATCTGCCTAGGTACATCGAAGTCTTTTGGACCTCCATACAGTGAATATGCCCTGTG  
ATCGCTGGTGGTATCCCTGGCGGCCCTTGCTCCCTGCTGTAGTGTGTGCTGCTCTGTCTTTACTTCAAAAATACACAAC  
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTGGCTGTAAAAAATCACAAACCAGACAAGGTGTGGTGGGCCAAG  
AACAGCCAGGGCCAAAACCATTGCCACGGAGTCTTTGTCTTCCCTGCGCTGCAAGGATATAGAATGTGTGCC  
AGTTTTGATTCCTTCCCTGCCACCTTGCTGTTGCGACATAAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA  
GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGT'TTGTGATGTGCAGGCACAGAAGAAGGCACAG  
CTCCCCATCAGTTTCATGGAAAATAACTCAGTGGCTGCTGGGAACCAAGCTGTGGAGATCCCTACAGAGAGCTTC  
CACTGGGGCCAAACCTTCCAGGAAGAGGTTGGGGAGGACCAACCTCACTGTGGGGAAATGCTGATAAACCAGTCA  
CACAGCTGCTCTATTTCTACACAAATCTACCCCTTGGCTGGCTGGAACCTGACGTTTCCCTGGAGGTGTCCAGAAA  
GCTGATGTAACACAGAGCCCTATAAAAGCTGTGCGTCCCTAAGGCTGCCAGCGCCTTGCCAAAATGAGAGCTTGTA  
AGAAGGCTCATGCCATTGACCCTCTTAATTCTCTCCGT'TTGGCGGAGCTGACAAATGGCGGAGGCTGAAGGCAAT  
GCAAGCTGCACAGTCAAGTCTAGGGGGTGGCAATATGGCAGAGACCCACAAGCCATGATCTTCCAATCAATCCC  
AGTGAGAACTGCACCTGGACAATAGAAAAGACAGAAAACAAAGCATCAGAATTATCTTTTCCCTATGTCCAGCTT  
GATCCAGATGGAAGCTGTGAAAGTGAAAACATTAAGTCTTTTGACGGAACCTCCAGCAATGGGCCCTCTGCTAGGG  
CAAGTCTGCAGTAAAAACGACTATGTTCCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTTACT  
GACTCAGCAAGAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCCTAACATCTCTATTCCAAACTGT  
GGCGGTTACCTGGATACCTTGGAAGGATCCCTTACCAGCCCCAATTACCCAAAGCCGCATCCTGAGCTGGCTTAT  
TGTGTTGGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAAACTTCAAAGAGATTTTCTAGAAAATAGAC  
AAACAGTGCAAATTTGATTTTCTTGGCATCTATGATGGCCCCCTACCAACTCTGGCCCTGATTTGGACAAGTCTGT  
GGCCGTGTGACTCCCACCTTCGAATCGTCAATAACTCTCTGACTGTCTGTGTGTCTACAGATTATGCCAATTTCT  
TACCGGGGATTTTCTGCTTCCCTACACCTCAATTTATGCAGAAAACATCAACACTACATCTTTAACTTGTCTTCT  
GACAGGATGAGAGTTATTTATAAGCAAATCCTACCTAGAGGCTTTTAACTCTAATGGGAATAAATTCGAACATAAAA  
GACCCAACTTTGCAGACCAAAATATCAAAATGTGTTGGAAATTTTCTGTCCCTCTTAAATGGATGTGGTACAATCAGA  
AAGGTAGAAGTCAAGTCAATTACTTACACCAATATAATCACCTTTTCTGCATCTTCAACTGTGAAGTGATCACC  
CGTCAGAAACCACTCCAGATTATTGTGAAGTGTGAAATGGGACATAAATCTACAGTGGAGATAATATACATAACA  
GAAGATGATGTAATACAAAGTCAAAATGCAC'TGGGCAAATATAACACCAGCATGGCTCTTTTTTGAATCCAATTCA  
TTTGAAAAGACTATAC'TTGAATCACCATA'TTATGTGGATTTGAACCAAACCTTTTTTGTTCAGTTAGTCTGCAC  
ACCTCAGATCCAAATTTGGTGGTGTTTCTTGATACCTGTAGAGCCTCTCCCACCTCTGACTTTTGCATCTGCCAAC  
TACGACCTAATCAAGATGGATGTAGTCGAGATGAAACTTGTAAAGGTGATCCCTTATTTGGACACTATGGGAGA  
TTCCAGTTTAAATGCCCTTTTAAATTTCTTGAGAAAGTATGAGCTCTGTGTATCTGCAGTGTAAAGTTTGTATGTGAT  
AGCAGTGAACACCAGTCTCGCTGCAATCAAGGTTTGTGTCTCCAGAAGCAAACGAGACATTTCTTTCATATAAATGG  
AAAACAGATTCCATCATAGGACCCATTTCGTCTGAAAAGGGATCGAAGTGCAGTGGCAATTCAGGATTTTCAGCAT  
GAAAACATATCGCGGAAGAACTCCAAACCAGCCCTTTCACAGTGTGCATCTGT'TTTTCTTTCATGGTTCTAGCTCTG  
AATGTGGTGTGACTGTAGCGCAATCACAGTGAGGCATTTTGTAAATCAACGGGCAGACATACAAATACCAAGAGCTG  
CAGAATCTATTAATCAACAGGTCCAACCTTAAGTGAGACATGTTTCTCAGGATGCCAAAGGAAATGCTACCTCGT  
GGCTACACATATTATGAATAAAATGAGGAAGGGCCTGAAAGTGACACACAGGCCTGCATGTAAAAAAA

## **FIGURE 70**

MELVRRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI  
ERPENKSIRIIFSIVQLDPDGSCSENIKVFDGTSSNGPLLQVCSKNDYVPVFESSSSTLT  
FQIVTDSARIQRTVFVFFYYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV  
EKDYKIKLNFKEIFLEIDKQCKFDLAIDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS  
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVVISKSYLEAFNSNGNNLQKDPCTCRP  
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGNST  
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN  
LVVFLDTCRASPTSDFASTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL  
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDSIIGPIRLKRDRSASGNSGFQHETHA  
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domain:**

amino acids 571-586

### **N-glycosylation site.**

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,  
394-398, 419-423

### **Casein kinase II phosphorylation site.**

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,  
408-412, 463-467, 520-524, 556-560

### **Tyrosine kinase phosphorylation site.**

amino acids 172-180, 407-415, 407-416, 519-528

### **N-myristoylation site.**

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG  
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGC  
TGCTGCCGCGCCGCGCGTGCCTGCCACAGCGCCACGCGCTTCGACCCACCTGGGAGTCC  
CTGGACGCCCCGCGAGCTGCCCGCGTGGTTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG  
GGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA  
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGAT  
TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAGTGGGCAGATATTTTTTCAGGC  
CTCTGGTGCCAAATACATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT  
CAGAATATTCGTGGAAGTGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA  
CTTGAGGTAGCCATTAGGAACAGAAGTACCTGCGTTTTGGACTGTACTATTCCCTTTTTGA  
ATGGTTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG  
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG  
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTT  
ATATAATGAAAGCCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA  
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA  
CATAAATGGGAAAAGTGCATGACAATAGACAACTGTCTGGGGCTATAGGAGGGAAGCTGG  
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG  
GAGGAAATCTTTTGATGAATATTGGGGCCACACTAGATGGCACCATTCTGTAGTTTTTTGAG  
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA  
TACCTGGCGATCCCAGAATGACACTGTCACCCCAGATGTGTGGTACACATCCAAGCCTAAAG  
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTTGGCCAT  
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAACTACTGGGCCATGGACAGCCACTTAACTG  
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTTCATCAGATGC  
CGTGTAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG  
ATGCTGCAAGTTATGTCTAAGGCTAGGAACTATCAGGTGTCTATAATTGTAGCACATGGAGA  
AAGCAATGTAACTGGATAAGAAAATTATTTGGCAGTTCAGCCCTTTCCCTTTTTTCCCACTA  
AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGCACTTTGCCATTAAAGTC  
TCTTCACATTGATTTGTTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTTCACATTATAGTAG  
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCATG  
ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT  
TTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA  
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG  
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG  
GTACAGTAAAAATACTGTAAAATAAATGGTGCACCTGTATAGGGCACTTACCACGAATGGAG  
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA  
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAA  
GTTTTTCTTTCTTCAATTATAAATTAACATAAGTGTACTGTAACTTTACAAACGTTTTAATT  
TTTAAAACCTTTTTGGCTCTTTTGTAATAACACTTAGCTTAAAACATAAACTCATTGTGCAA  
ATGTAA

## **FIGURE 72**

MRPQELPRLAFPLLLLLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG  
VFSVPSFGSEWFWWYWQKEKIPKYVEFMKDNYPFSFKYEDFGPLFTAKFFNANQWADIFQAS  
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEW  
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY  
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI  
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT  
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI  
SLEQNGIMVELPQLTIHQMPCKKGWALALTNVI

### **Signal sequence:**

amino acids 1-28

### **N-glycosylation site.**

amino acids 171-175, 239-243, 377-381

### **Casein kinase II phosphorylation site.**

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,  
375-375

### **Tyrosine kinase phosphorylation site.**

amino acids 361-369, 389-397

### **N-myristoylation site.**

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

### **Leucine zipper pattern.**

amino acids 410-432

### **Alpha-L-fucosidase putative active site.**

amino acids 283-295

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## FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT  
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC  
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG  
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT  
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACCAGC  
AGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG  
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGAGGA  
TGGATTTCGTGGTCATCTCTAGGATTAGCCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG  
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT  
ACTTGGACTAACTCGTGCATTTCCAGAAATTATCACCACCAAAGATCCCATATTCAACACTCA  
AACTGCAACACAAACAACAGAATTTATTGTGAGTGACAGTACCTACTCGGTGGCATCCCCTT  
ACTCTACAATACCTGCCCCTACTACTCTCCTGCTCCAGCTTCCACTTCTATTCCACGG  
AGAAAAAAATTGATTTGTGTACAGAAGTTTTTATGGAACTAGCACCATGTCTACAGAAAC  
TGAACCATTTGTTGAAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTTGGAGGTGTCC  
CCACGGCTCTGCTAGTGCTTGCTCTCCTCTTCTTTGGTGCTGCAGCTGGTCTTGGATTTTGC  
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT  
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA  
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCGATGCCTGGAA  
GCTGAAGTTTATAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGCTCC  
TTACCCTGCCCCAGCTGGGGAAATCAAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCCTT  
GGTTCCTAAGTGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC  
CCTTCTCCTTATTGTAACCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC  
TTTCTAGCCTGGCTATGTCCTAATAATATCCCACTGGGAGAAAGGAGTTTTTGCAAAGTGCAA  
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCTCCTGGCTGTCTGAGGCTAGG  
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTTCTCTACTGATTCCGCAGCTCAGAC  
CCTTTCTTCAGCTCTGAAAGAGAAACACGTATCCCACTGACATGTCTTCTGAGCCCGGTA  
AGAGCAAAAGAATGGCAGAAAAGTTTAGCCCCTGAAAGCCATGGAGATTCTCATAACTTGAG  
ACCTAATCTCTGTAAAGCTAAAATAAAGAAATAGAACAAGGCTGAGGATACGACAGTACACT  
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTTTTCTCTGAACACATTGAGTTGGA  
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTACCACTGCTGATATTTTCTCT  
AGGAAATATACTTTTACAAGTAACAAAAATAAAAACTCTTATAAATTTCTATTTTTTATCTGA  
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAAATTCA  
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT  
TGAATATTATTCTCAAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTTTTTTTCA  
GTTTTGATATTTCTAGCTTATCTACTTCCAACTAATTTTTTATTTTTGCTGAGACTAATCTT  
ATTCAATTTTCTCTAATATGGCAACCATTATAACCTTAATTTATTATTAACATACCTAAGAAG  
TACATTGTTACCTCTATATAACCAAAGCACATTTTAAAAGTGCCATTAACAAATGTATCACTA  
GCCCTCCTTTTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTTGTGACAAAAAATTAA  
AGCATTTAGAAAACCTT

## **FIGURE 74**

MARCFSLVLLLTSIWTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR  
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQF  
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP  
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPTALLVLALLFF  
GAAAGLGFCYVKRYVKAFPFNTKNQOKEMIETKVVKEEKANDSNPNEESKKTDKNPPEESKSP  
SKTTVRCLEAEV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 235-254

### **N-glycosylation site.**

amino acids 53-57, 130-134, 289-293

### **Casein kinase II phosphorylation site.**

amino acids 145-149, 214-218

### **Tyrosine kinase phosphorylation site.**

amino acids 79-88

### **N-myristoylation site.**

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

## FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTGTATTGCGGTGCCGCGACTTTCACGATGG  
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAA  
ACTGCCGCGCTCTGCCACGGTCTGCCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTG  
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA  
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT  
TCTTTTCTTCCGCTTGGATATTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTCC  
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA  
ACCATTGATGAGGAAC TAGAACGGGACAAGAGGGTCAC TTGGATTGTGGAGTTCTTTGCCAA  
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC T  
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC  
AAAGTGAGCACATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA  
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG  
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA  
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGT CAGA  
TGGGGAAAACAAGAAGGATAAA TAAGATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATT  
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGG  
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG  
GCACCTTACAGGAAGGCCTGCCATGCTGTGGCCAAC TGTTCCTGAGCAAGAAAGAGATC  
TCATAGGACGGAGGGGGAAATGGTTTCCCTCCAAGCTTGGGTCAGTGTGTTAACTGCTTATC  
AGCTATTCAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCTTCTTAG  
TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAA  
CGCTAAGAATTTTCCCCCAAGGACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTC  
TTCATTAAAAGTATAAGCCTAACTTTGTCGCTAGTCCTAAGGAGAAACCTTTAACCACAAAG  
TTTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA  
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGAGAGGAGAAATCCCTGGACTTTCAC  
TAACCTCTGACATACTCCCCACACCCAGTTGATGGCTTTCCGTAATAAAAAGATTGGGATT  
TCCTTTTG

## **FIGURE 76**

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLRKLPPLCHGLPTQREDGNPCDFD  
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL  
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC  
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE  
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

### **Signal sequence:**

amino acids 1-48

### **Transmembrane domain:**

amino acids 111-125

### **N-glycosylation site.**

amino acids 165-169, 185-189

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 154-158, 265-269

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

### **N-myristoylation site.**

amino acids 188-194, 225-231

### **Myb DNA-binding domain repeat signature 1.**

amino acids 244-253

## FIGURE 77

GGACAGCTCGCGGCCCCCGAGAGCTCTAGCCGTGAGGAGCTGCCTGGGGACGTTTGCCCTG  
GGGCCCCAGCCTGGCCCCGGGTCAACCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCCA  
TTGCTCCTGCTGCCCCGGCTCCTACGGACTGCCCTTCTACAACGGCTTCTACTACTCCAACAG  
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG  
TGGTGGAGACACCCGAGGAGACCCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC  
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGGAAAGCT  
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT  
TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG  
ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGA  
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCCTTACCAGTCCCCCA  
ACGGGCGCTACCAGTTCAACTTCCACGAGGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG  
GTGGCCTCCTTTGAGCAGCTCTTCCGGGCCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG  
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCCGGCAGCCCTGCGGTGGCC  
CAGGCCTGGCACCTGGCGTGCGAAGCTACGGCCCCCGCCACCGCCGCTGCACCGCTATGAT  
GTATTCTGCTTCGCTACTGCCCTCAAGGGGCGGGTGTACTACCTGGAGCACCCCTGAGAAGCT  
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGAC  
AGCTCTTTGCCGCTGGAAGTTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT  
GGCAGCGTCCGCTACCCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCCAGAGCCTGGGGT  
CCGAAGCTTTGGCTTCCCCGACCCGCAGAGCCGCTTGTACGGTGTTTACTGCTACCGCCAGC  
ACTAGGACCTGGGGCCCTCCCCTGCCGCATTCCCTCACTGGCTGTGTATTTATTGAGTGGTT  
CGTTTTCCCTTGTGGGTTGGAGCCATTTTAACTGTTTTTTATACTTCTCAATTTAAATTTTCT  
TTAAACATTTTTTTTACTATTTTTTTGTAAAGCAAACAGAACCCAATGCCTCCCTTTGCTCCTG  
GATGCCCCACTCCAGGAATCATGCTTGCTCCCCCTGGGCCATTTGCGGTTTTGTGGGCTTCTG  
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCCAGAGTGGGC  
GGTGGCCTGTCTAGAATGCCGCCGGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCCT  
CAGCCTGGGGGAAGAAGAGGGCCTCGGGGGCCTCCGAGCTGGGCTTTGGGCCTCTCCTGCC  
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAA  
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAACTCCCCTCCCCGTTCCCCT  
TCCCCTCTCGGTTCCAAAGAATCTGTTTTTGTGTGTCATTTGTTTTCTCCTGTTTTCCCTGTGTGG  
GGAGGGGGCCCTCAGGTGTGTGTACTTTGGACAATAAATGGTGTCTATGACTGCCTTCCGCCAA  
AA  
AA

## **FIGURE 78**

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ  
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD  
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ  
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR  
HRRLLHRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDR  
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

### **Signal sequence:**

amino acids 1-17

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 53-57, 111-115, 278-282

### **Tyrosine kinase phosphorylation site.**

amino acids 137-145

### **N-myristoylation site.**

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

## FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC  
TTCTGTTGCTACTGAGGCACGGGGCCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC  
CAGGGGAGGGTGCACCAGGCGGCCCCCTGAGCGACGCTCCCCATGATGACGCCCACGGGAA  
CTTCCAGTACGACCATGAGGCTTTCCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA  
CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC  
GGCGACGGCTGGGTGTCGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA  
CATACGGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG  
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGAC  
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC  
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG  
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCCTGGAGGACCTGGACAGAAACAA  
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA  
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGGACTTCCGGGATCTGAACAAGG  
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCCAGGACCAGCCC  
CTGGTGGAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA  
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG  
ACCTGACCCGGCACCACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCCG  
CACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGCAGGAG  
GCAGATGCAGTCCCAGGCATCCTCCTGCCCCCTGGGCTCTCAGGGACCCCCTGGGTGCGCTTC  
TGTCCCTGTCACACCCCCAACCCCAGGGAGGGCTGTCTAGTCCCAGAGGATAAGCAATAC  
CTATTTCTGACTGAGTCTCCCAGCCCAGACCCAGGGACCCTTGGCCCCAAGCTCAGCTCTAA  
GAACCGCCCCAACCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCCT  
GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA  
AAGCCAGCGCCGGGACCTTGAAA  
AAAAAAAAAAAAAAAAA

## **FIGURE 80**

MMWRPSVLLLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR  
EVAKEFDQLTP EESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT  
YDTRDGRVGVWHEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGD SMATRE  
ELTAFLHP EEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEP AWVQTERQQ  
FRDFRDLNKDGHLDGSEVGHWVLPPAQDQPLVEANHLLHESD TDKDGRLSKAEILGNWNMFV  
GSQATNYGEDLTRHHDEL

### **Signal sequence:**

amino acids 1-20

### **N-glycosylation site.**

amino acids 140-144

### **Casein kinase II phosphorylation site.**

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,  
291-295, 298-302

### **N-myristoylation site.**

amino acids 263-269, 311-317

### **Endoplasmic reticulum targeting sequence.**

amino acids 325-330

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## FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG  
GCGGCGGGGCGCGGGTGCAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTCGCTCCCAG  
CCTGTCTGTCTGTCGTTTGGCGCCCCCGCTCCCCGCGGTGCGGGGTGCACACCGATCCTG  
GGCTTCGCTCGATTTGCCGCCGAGGCGCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG  
CGGGTCGTCTGTCTCTCTCTCTCTGCGCCGCGCCGGGGATCCGAAGGGTGCGGGGCTCT  
GAGGAGGTGACGCGCGGGGCTCCCGCACCTGGCCTTGCCCGCATTTCTCCCTCTCTCCCAG  
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCCGGCTCTCGGCCTCGGTGTG  
TGTCTGCTGCTGCTGCCGGGGGCCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG  
TTTTACCAGAGGCTTGGACATCAGGAAAAGAGAAAGCAGATGTCCTCTGCCCAGGGGGCTGCC  
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG  
GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC  
TGGTCGAGAAAACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGAT  
GGTCTGCTTCTTTTACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA  
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGG  
CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGC  
GCCGATTTAATTTACAGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACA  
GAAGGACCACATGTGGGCCTTGTTCAAGCCAGTGAACATCCCAAATAGAATTTTACTTGAA  
AACTTTACATCAGCCAAAGATGTTTTGTTTGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA  
ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGA  
GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACAT  
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA  
AGCCTATCCCTGAAGAAGTGGGGATGGTTTCAAGATGTCACATTTGTTGACAAGGCTGTCTGT  
CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAAA  
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGTCAGCAAGACCTGTTATAACT  
CAGTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC  
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAAATCTCGGACATTGGTGCCAAGAT  
AGCTGCTGTACAGTTTACTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACCA  
AAGAGAATGTCCTAGCTGTCTATCAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT  
GATGCCATTTCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAAGAA  
CTTCTAGTAATTGTACAGATGGGCAGTCTATGATGATGTCCAAGGCCCTGCAGCTGCTG  
CACATGATGCAGGAATCACTATCTTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG  
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTTCTTACAAGAGAGTTCACAGGATT  
AGAACCAATTGTTTCTGATGTCATCAGAGGCATTTGTAGAGATTTCTTAGAATCCCAGCAAT  
AATGGTAACATTTTGACAAGTGAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTGTATT  
CTCATAATACTGAAATGCTTTAGCATACTAGAATCAGATACAAAACCTATTAAGTATGTCAAC  
AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT  
ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA  
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAAA  
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAAAA

## **FIGURE 82**

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEFVY  
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVTVT  
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN  
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRGGNSNTGKAL  
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG  
MVQDVTTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNVNI AFLI  
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI  
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI  
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

### **Signal sequence:**

amino acids 1-24

### **N-glycosylation site.**

amino acids 100-104, 221-225

### **Casein kinase II phosphorylation site.**

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,  
425-429, 478-482, 528-532

### **N-myristoylation site.**

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,  
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

### **Amidation site.**

amino acids 145-149

## FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCCGCCACCGCGCCGCTCCCGCATCTGCACCCGCAGCCC  
GGCGGCCTCCCGGCGGGAGCGAGCAGATCCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG  
GGGCGGCGGCTGCGGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCCACCCTGCTGTGCCTGC  
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC  
AAGCCCGGCCCGGCTCTCAGCTACCCGCAGGAGGAGGCCACCCTCAATGAGATGTTCCGCGA  
GGTTGAGGAACTGATGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG  
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCCAGCTAT  
CACAATGAGACCAACACAGACACGAAGGTTGGAAATAATACCATCCATGTGCACCGAGAAAT  
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG  
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCCAGC  
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT  
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA  
TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGGCTG  
TGCTGTGCCCTTCCAGAGAGGCCTGCTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA  
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG  
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG  
GTGTATGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC  
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG  
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCCTGCGGCTGCCGCCGCT  
GCACTGCTGGGAGGGGAAGAGATTTAGATCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA  
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTTCCTACA  
TCTTCTTCCCAGTAAGTTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGC  
TCCCCCAGGCTGTTCTCCAGGCTTACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC  
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG  
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGG  
AGTCTCCCTCTGATTGGTTTTGGGGAAATGTGGAGAAGAGTGCCTTGCTTTGCAAAATCAA  
CCTGGCAAAAATGCAACAAATGAATTTTCCACGCAGTTCTTTCCATGGGCATAGGTAAGCTG  
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTACCCTGCATTACATGTGTTTATTCATCC  
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTTCATATCCAAGATCAATTC  
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCAATTGTTCTCCTCGTCCATCAGGGATCTCAGAG  
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTTTCAT  
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA  
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTTCTTGAGGCATGCACATCTGGAATTAAG  
GTCAAACATAATTCTCACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC  
AGTGTGGGGCAGCCGTCCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT  
TGCATTAGTAACCTTTGAAAGGTATATGACTGAGCGTAGCATAACAGTTAACCTGCAGAAACA  
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC  
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT  
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTTCAGGTGTCA  
TGGACTGTTGCCACCATGTATTTCATCCAGAGTTCTTAAAGTTTAAAGTTGCACATGATTGTA  
TAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTGCATTTAGAAATCAAGC  
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 84**

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ  
HKLRS AVEEMEAEEAAKASSEVNLANLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG  
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDSECCG  
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL  
LDLITWELEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV  
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGEEI

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 96-100, 106-110, 121-125, 204-208

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,  
327-331

### **N-myristoylation site.**

amino acids 202-208, 217-223

### **Amidation site.**

amino acids 140-144

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[illegible]

АААА

## **FIGURE 86**

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA  
VPPALPAGTQTLLQLSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL  
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE  
MLPNLEILMIGGNKVDAILDMNFRPLANLRSLVLAGMNLREISDYALEGLQSLESLSFYDNQ  
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIKDFALVNL  
ELTKLDITNNPRLSFIHPRAFHLPQMETLMLNNALSALHQQTVESLPNLQEVGLHGNPIR  
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ  
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAEAGLYT  
CVAQNLVGADTKTVSVVVGRALLQGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW  
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS  
CHRALGDRPGLIAILALAVLLLAAGLAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSRRVV  
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 629-648

### **N-glycosylation site.**

amino acids 94-98, 381-385, 555-559, 583-587

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 485-489

### **Casein kinase II phosphorylation site.**

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,  
243-247, 313-317, 488-492, 700-704

### **Tyrosine kinase phosphorylation site.**

amino acids 532-540

### **N-myristoylation site.**

amino acids 15-21, 493-499, 566-572

### **Amidation site.**

amino acids 470-474, 660-664, 692-696

## FIGURE 87

GCAAGCCAAGGCGCTGTTTTGAGAAGGTGAAGAAGTTCGGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT  
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA  
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCCACCC  
CCTGGCCACACTCTTCAAGATCCTGGCGTCCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA  
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAACTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG  
CGACATCCCCGACGTCAAGAACGACTTCGCCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA  
GCGCTTCGCCGTCTTCTGTGCGAGGTGAGTGAGAACAAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT  
GGACAAGCTCCGGCAGCGGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT  
CCCTGACACTGTGTTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC  
CAGCATTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT  
GGCCTTCTGCGCGAGAACCCTGCGGGCGCTGCACATCAAGTTTACCGACATCAAGGAGATCCCGCTGTGGATCTA  
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACCAACCGCTACATCGTCATCGA  
CGGGCTGCGGGAGCTCAAACGCCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC  
AGATGTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCACCAAGCTCATCGTCTTCAACAGCCTCAA  
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCCACTCCATCTTCAGCCT  
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT  
GCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA  
CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGCAAGCTGCG  
CTACCTGGACCTCAGCCACAACAACCTGACCTTCTCCCTGCCGACATCGGCCTCCTGCAGAACCTCCAGAACCT  
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT  
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGTGGGCGAGCTGACCAACCTGACGCAGATCGAGCTGCGGGG  
CAACCGGCTGGAGTGCTTGCCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA  
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGGAG  
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGAGGGGCGAGGCTAGCTTCTCCAG  
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGGCCGCTTGTGAGTCAGGCCAGAGCGGAGA  
GGACAGTATCTGTGGGGCTGGCCCCCTTTTCTCCCTCTGAGACTCACGTCCCCAGGGCAAGTGCTTGTGGAGGAG  
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG  
CTGCCACCAGAGGTCTGGGACCCCTCACTTTAGTTCTTGGTATTTATTTTCTCCATCTCCCACCTCCTTCATCC  
AGATAACTTATACATTCCCAAGAAAGTTTACGCCAGATGGAAGGTGTTTCAAGGAAAGGTGGGCTGCCTTTTCCCC  
TTGTCCTTATTTTAGCGATGCCGCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCCAG  
CCATGGGACGGTCACCCAGCAGTGCCGGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCTCCAGCTGGA  
AAGGCCAGGCCTGGAGCTTGCCTCTTTCAGTTTTTTGTGGCAGTTTTAGTTTTTTGTTTTTTTTTTTAAATCAAA  
AAACAATTTTTTTTTTAAAAAAGCTTTGAAAATGGATGGTTTTGGGTATTAAGGAGAAAAAAGCTTAAAAA  
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAGCAGCCAGACGT  
TGAAGTGTGTTTTCTTTCCCTGGGCGCAGGGTGCAGGGTGTCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTT  
CTATTTGTTTCTGGGGAGGGAGGTTTTTTTTGTTTTTTTTTGGGTTTTTTTTTGGTGTCTTGTCTTTCTTCTCCCTCC  
ATGTGTCTTGGCAGGCACCTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG  
ACTCGGGTTGGCTAATCCCCGATGAACGGTGTCTCATTCGCACCTCCCCTCCTCGTGCCTGCCCTGCCTCTCCA  
CGCACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGCCCAGACTTTGTTTTCCCCACCTCCTGCGGCATGGGTGTGT  
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCACCTGGTCCCTCATGAAGAGCAGACACTTA  
GAGGCTGGTCCGGAATGGGGAGGTGCGCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGGTTCCCGTCCCTGGCGC  
CTGGAGTGACACAGCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT  
AGAAGGGTCCCCGCTTAGATCAATCAGTGGACACTAAGGCACGTTTTAGAGTCTCTTGTCTTAATGATTATGT  
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTCTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG  
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAAA  
ATCTATAACAGAAAAA

## **FIGURE 88**

MRQTIKVIKFILLICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI  
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK  
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHLFMLSGIPDPTVFDLVELEV  
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWI  
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI  
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIISFQ  
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKRLRYLDLSHNNLT  
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHLGNNVLQSLPSRVGELTNLTQIE  
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

### **Transmembrane domain:**

amino acids 51-75 (type II)

### **N-glycosylation site.**

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 85-89

### **Casein kinase II phosphorylation site.**

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,  
398-402, 493-497

### **N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

## **FIGURE 89**

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCAATGGAGCTGGCACTGCGGCGCTCTCCCGT  
CCCGCGGTGGTTGCTGCTGCTGCCGTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT  
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG  
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCCCTGGTCAT  
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTTGGAACTTTGAGGAAATTGGGC  
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT  
GTGGATAATCCCGTGGGCACTGGGTTCACTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA  
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG  
AATTCAGACAGTTCCATTCTACATTTTCTCAGAGTCCTATGGAGGAAAAATGGCAGCTGGC  
ATTGGTCTAGAGCTTTATAAGGCCATTCAGCGAGGGACCATCAAGTGCAACTTTGCGGGGGT  
TGCCTTGGGTGATTCTCTGGATCTCCCCTGTTGATTTCGGTGCTCTCCTGGGGACCTTACCTGT  
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA  
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT  
GATCATTGAACAGAACACAGATGGGGTGAAGTTCTATAACATCTTAACTAAAAGCACTCCCA  
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGCCACCTAGTTTGTCTTTGTCAGCGC  
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA  
GCTCAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA  
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC  
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAGGAGGCCTG  
GGTGCGGAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGGAAAGGCCCTGT  
ACAGTGACCCTAAATCTTTGGAAACATCTGCTTTTGTCAAGTCCTACAAGAACCTTGCTTTC  
TACTGGATTCTGAAAGCTGGTCATATGGTTCTTCTGACCAAGGGGACATGGCTCTGAAGAT  
GATGAGACTGGTGACTCAGCAAGAATAGGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT  
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT  
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT  
GGAGGCAATTTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT  
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

## **FIGURE 90**

MELALRRSPVPRWLLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC  
KNFSELPVVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY  
VNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR  
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAV NKGLYRE  
ATELWGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS  
QLMNGPIRKKLKIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL  
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP  
SDQGDMAKMMRLVTQQE

### **Signal sequence:**

amino acids 1-25

### **N-glycosylation site.**

amino acids 64-68, 126-130, 362-366

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 101-105

### **Casein kinase II phosphorylation site.**

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

### **N-myristoylation site.**

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,  
187-193, 195-201, 331-337, 332-338, 360-366

## **FIGURE 91**

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC  
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA  
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA  
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG  
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG  
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG  
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCCTATGACATTG  
CCTTGGTGAAGCTGTCTGCACCTGTCACCTAACTAAACACATCCAGCCCATCTGTCTCCAG  
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA  
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTCGCCATCATAAACA  
ACTCTATGTGCAACCACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG  
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCTT  
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG  
GTCGGCCCAATCGGCCCCGGTGTCTACACCAATATCAGCCACCACCTTTGAGTGGATCCAGAAG  
CTGATGGCCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTTTCCCTCT  
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTTGAGCCTACCTGAGCCCATGCAGCCTGGGGC  
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTTGTTTGGTAATAAACACATTCCAGTTGA  
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 92**

MGARGALLLALLLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW  
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI  
YLSPRYLGNSPYDIALVKLSAPVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP  
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG  
LWYQIGVVSWGVCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFFPLLWALPL  
LGPV

### **Signal sequence:**

amino acids 1-18

### **N-glycosylation site.**

amino acids 167-171, 200-204, 273-277

### **Casein kinase II phosphorylation site.**

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

### **N-myristoylation site.**

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,  
259-265, 269-275

### **Amidation site.**

amino acids 33-37

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 252-263,

### **Serine proteases, trypsin family, histidine active site.**

amino acids 78-84

## FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT  
CTTTGCCCTCATCCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCGACCAGCGGAGGACGC  
TGCCCCCAGGCTGGGTGTCCCTGGGCGGTGCGGACCCTGAGGAAGAGCTGAGTCTCACCTTT  
GCCCTGAGACAGCAGAATGTGGAAGACTCTCGGAGCTGGTGCAGGCTGTGTTCGGATCCCAG  
CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC  
CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCAGAAAGTGCCATTCT  
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC  
TGGGGCTGAGTTTTCATCACTATGTGGGAGGACCTACGGAACCCATGTTGTAAGGTCCCCAC  
ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCGT  
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT  
GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAGCGATACTTACCTCACAAGACGTGG  
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCTGGAGCAGTATTTCCATGAC  
TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC  
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCGGGGATTGAGGCCAGTCTAGATGTGCAGT  
ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG  
GGACAGGAGCCCTTCTGCAGTGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT  
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA  
ACACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCCTGCTCTTCGCCTCAGGTGACAGT  
GGGGCCGGGTGTTGGTCTGTCTCTGGAAGACACCAGTTCGCCCCCTACCTTCCCTGCCTCCAG  
CCCCATATGTCACCACAGTGAGGAGCACATCCTTCCAGGAACCTTTCCTCATCACAATGAAA  
TTGTTGACTATATCAGTGCTGGTGGTCTTCAGCAATGTGTTCCACAGGCCTTCATACCAGGAG  
GAAGCTGTAACGAAGTTCCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC  
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTCTGATGGCTACTGGGTGGTCAGCAACA  
GAGTGCCCATTCATGGGTGTCCGGAACCTCGGCCTCTACTCCAGTGTTTGGGGGGATCCTA  
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACCCAAG  
GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC  
TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGC  
TGGGGAACACCAACTTCCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCTCTATC  
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCAGTCCCTTATTCTGCCCTGTTG  
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCTGAAA  
TGCTGTGAGCTTGACTTGACTCCCAACCCTACCATGCTCCATCATACTCAGGTCTCCCTACT  
CCTGCCCTTAGATTCTCAATAAGATGCTGTAACCTAGCATTTTTTTGAATGCCTCTCCCTCCGC  
ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA  
TTTCACTTGATATTCAATCCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTTACTCT  
TTCCTACCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTTGCTTTATG  
GCCTTTCCATCATAGTTGCCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACTTCTCTG  
ACTACTCTTGTCTTCTCTCTCATCAATTTCTGCTTCTTCATGGAATGCTGACCTTCATTGC  
TCCATTTGTAGATTTTTGCTCTTCTCAGTTTACTCATTTGTCCCCTGGAACAAATCACTGACA  
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAA  
TGTAACAAAA

## **FIGURE 94**

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS  
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL  
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP  
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG  
GNFAHQASVARVVGGQQGRGRAGIEASLDVQYILMSAGANISTWVYSSPGRHEGQEPFLQWLML  
LSNESALPHVHTVSYGDDDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH  
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP  
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG  
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGGFCSGPGWDPVTGWGTPTSQLC

### **Signal sequence:**

amino acids 1-16

### **N-glycosylation site.**

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

### **Glycosaminoglycan attachment site.**

amino acids 361-365, 408-412, 538-542

### **Casein kinase II phosphorylation site.**

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

### **N-myristoylation site.**

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,  
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,  
521-527, 533-539, 549-555

[illegible][illegible]

## **FIGURE 96**

MAGIPGLLFLLFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS  
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSGSSGKS  
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG  
TQKL RVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA  
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD  
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQICYW  
IKGNYLDCREG

### **Signal sequence:**

amino acids 1-19

### **N-glycosylation site.**

amino acids 93-97, 207-211

### **Glycosaminoglycan attachment site.**

amino acids 109-113, 316-320

### **Casein kinase II phosphorylation site.**

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

### **N-myristoylation site.**

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

### **Serine proteases, trypsin family, histidine active site.**

amino acids 171-177

## **FIGURE 97**

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT  
CTGGAGCGCCCCAGCCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG  
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA  
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA  
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC  
ACTGCTGCCCCACTGTTTCAAGGACAACCTGAACAAACCATACTGTTCTCTGTGCTGCTGGG  
GGCCTGGCAGCTGGGGAACCCCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC  
CCCACCCTGTGTATTCTTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCTCGAG  
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT  
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCCTTGC  
CCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT  
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT  
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG  
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC  
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA  
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG  
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA  
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCCGTAAATAGGCTCATCTACC  
TCTACCTCTGGGGGCCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCGAC  
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCCGCCAACGGCCTCATGTCCCCGCCCCAC  
GACTTCCGGCCCCCGCCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTTAT  
AGGTATTTGTAACCCTGCCCACATATCTTATTTATTCCTCCAATTTCAATAAATTATTTATT  
CTCCAAAAAAAAA

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318

><subunit 1 of 1, 317 aa, 1 stop

><MW: 33732, pI: 7.90, NX(S/T): 1

MVVGAPPALGGGCLGTFTSLLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP  
WIVSIQKNGTHHCAGSLLTSRWVITAACHCFKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGVA  
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPNTHCWISGWGSIQDG  
VPLPHPQTLQKLKVPIDSEVCSHLYWRGAGQGPITEDMLCAGYLEGERDACLGDSGGPLMC  
QVDGAWLLAGIISWGECAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG  
SGAAARS

### **Signal sequence:**

amino acids 1-32

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

## FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCCTGATGCTTCTGCTGCCGCTACTGCTA  
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT  
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA  
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC  
AACAAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCCGCCATCACAGACGAGGGCATGGACGT  
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT  
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC  
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT  
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC  
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC  
CCGGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGA  
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT  
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC  
CCAACCTTCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC  
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGATGAGGAGCCAGTTA  
CCTTCCCCAAATCGACCCATGTTCTATCCCAAAATCAGCAGACAAAGTGACAGACAAAACA  
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG  
GGAACCTCTACCCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG  
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC  
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAA  
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCCTTGCCAGGTGCAGAGGGGCCCTGACA  
AGCCTAGCGTTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA  
CTACTGCTCCTGCCTCCTCTGGTGTGTTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG  
TGAAGAGGTGAGCTGTCTCCTGTGTCATCTTCCCCACCCTGTCCCCAGCCCCCTAAACAAGATA  
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC  
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCCTGAGGACTGCACACC  
GGGCCCACACCTCTCCTGCCCCCTCCCTCCTGAGTCCTGGGGGTGGGAGGATTTGAGGGAGCT  
CACTGCCTACCTGGCCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG  
TGTAGCTGGGGATGGGGATTCTAGGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGGTTTC  
TTTGAGTGGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT  
GTCCAACCTGTGAAA

## **FIGURE 100**

MHGSCSFLMLLLPLLLLLLVATTGPVGALTDEEKRLMVELHNLVYRAQVSPTASDMLHMRWDEE  
LAAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ  
MCGHYTQVWAKTERIGCGSHFCEKLQGVETNIELLVVCNYEPPGNVKGKRPYQEGTPCSQC  
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRAEASDSRKMGTTPSSLATGIPAFVTEV  
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKS  
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEAEELPPSSEVLAS  
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGPDKPSVV  
SGLNSGPGHVWGPLLGLLLLLPPLVLAGIF

### **Signal sequence:**

amino acids 1-22

### **N-glycosylation site.**

amino acids 114-118, 403-407, 409-413

### **Glycosaminoglycan attachment site.**

amino acids 439-443

### **Casein kinase II phosphorylation site.**

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

### **N-myristoylation site.**

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,  
250-256

### **Amidation site.**

amino acids 82-86, 172-176

### **Peroxidases proximal heme-ligand signature.**

amino acids 287-298

### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.**

amino acids 127-138

### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.**

amino acids 160-172

## FIGURE 101

GTAAGTGAAGTCAGGCTTTTCATTTGGGAAGCCCCCTCAACAGAATTTCGGTCATTCTCCAAGTTATGTTGGACGT  
ACTTCTGTTGTTCTCCCTCTGCTTGTCTTTTTCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTTTCAT  
CAAGGCAAGTTCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCC  
AAATCTGGGACCAGTCTCGGCAAAATATACACTTCTCTCTTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA  
ACATCTGAAAGAGTTTTCAGTCCCTTGAACCTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATT  
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAA  
TTTGGCCAACACACTCCTTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAGATGTTTAAACT  
GCCCCAAGTGAACATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTCCAAGGCCTTGG  
TGCTCTGAAGTCTCTGAAAATGCAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTTTGGGGGCTGAGCAA  
CATGGAATTTTGCAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCT  
GCAGGAACCTCATCTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCTGGGAGTTCTGCCAGAAGCTCAG  
TGAGCTGGACCTAACTTTCAATCACTTATCAAGTTAGATGAATTCAGCTTCCTTGGCCTAAGCTTACTAAATAC  
ACTGCACATTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCCCTTCCGGGGGCTTTCCAGTTTAAAGACTTT  
GGATCTGAAGAACAATGAAATTTCTTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAAACTGAG  
GCGACTGATACTCCAAGGAAATCGGATCCGTTCCTATTAATAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCA  
TCTAGACCTGAGTGACAACGCAATCATGTCTTTACAAGGCAATGCATTTTCAAAATGAAGAAAAGTGAACAAT  
GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAAATGGCTCCACAGTGGGTGGCGGAAAACAACAT  
TCAGAGCTTTGTAAATGCCAGTTGTGCCCATCCTCAGCTGCTAAAAGGAAGAAGCATTTTGTCTGTTAGCCGAGA  
TGGCTTTGTGTGTGATGATTTTCCCAAACCCAGATCACGGTTTCAGCCAGAAACACAGTCGGCAATAAAAGGTTT  
CAATTTGAGTTTTCATCTGCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTTGCTTGAAAAAAGACAATGA  
ACTACTGCATGATGCTGAAATGGAAAAATATGCACACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCA  
CATCCTTCGGCTGCGCGAGGTGGAATTTGCCAGTGAGGGGAAAATATCAGTGTGTCTCTCAATCACTTTGGTTC  
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCAT  
CCGAGCTGGGGCCATGGCACGCTTGGAGTGTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAAGGA  
TGGGGGCACAGACTTCCAGCTGCACGGGAGAGACGCGATGCATGTGATGCCCCGAGGATGACGTGTTCTTTATCGT  
GGATGTGAAGATAGAGGACATTGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAAATGC  
AACTCTGACTGTCTTAGAAACACCATCATTTTTCGCGCCACTGTGGACCGAACTGTAAACCAAGGGAGAAACAGC  
CGTCTACAGTGCAATGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTTGGTGGT  
AACCAGAGAGGCATTTTTTTCAGCAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTGATGCTGGGAA  
ATACACATGTGAGATGTCTAACACCCCTTGGCACTGAGAGAGGAAACGTCGCGCTCAGTGTGATCCCCACTCAAC  
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCTGTATCATAGC  
CGTGGTTTGTGTGTGGTGGGCACGTCACTCGTGTGGGTGGTTCATCATATACCACACAAGGCGGAGGAATGAAGA  
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCCTAGTTATTTGTCTCATCTCAGGGAACGTT  
AGCTGACAGGCAGGATGGGTACGTGTCTTCAGAAAGTGGAAGCCACCACAGTTTGTACATCTTCAGGTGCTGG  
ATTTTTCTTACCACAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGC  
CACAGATCTGTTCCTTTGTCCGTTTTTGGGATCCACAGGCCCTATGTATTTGAAGGGAAATGTGTATGGCTCAGA  
TCCTTTTGAACATATCATACAGGTTGCAGTCTTACCCAAAGAACAGTTTAAATGGACCACTATGAGCCAGTTA  
CATAAAGAAAAAGGAGTGCTACCCATGTTCTCATCTTCAGAAAGATCCTGCGAACGGAGCTTCAGTAATATATC  
GTGGCCTTTCATGTGTGAGGAAGCTACTTAACACTAGTTACTCTCAATGAAGGACCTGGAATGAAAAATCTGTG  
TCTAAACAAGTCCTCTTTAGATTTTAGTGCAATCCAGAGCCAGCGTCGGTTGCCCTCGAGTAATTTCTTTCATGGG  
TACCTTTGAAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTTCAGCTTTGGACAGCCATCAGATTGTTCAGCC  
AAGAGCCTTTTATTTGAAAGCTCATTCTTCCCCAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGAC  
AGATTTTCAGGAAGAAATCACATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGTC  
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTTATTTA  
AAAGAGAGAGAATCTTATGTTTTTTAAATGGAGTTATGAATTTTAAAAGGATAAAAAATGCTTTATTTATACAGAT  
GAACCAAAATTAACAAAAGTTATGAAAAATTTTATACTGGGAATGATGCTCATATAAGAAATACCTTTTTTAAACTA  
TTTTTTAACTTTGTTTTATGCAAAAAAGTATCTTACGTAATTAATGATATAAATCATGATTATTTATGTATTT  
TTATAATGCCAGATTTCTTTTTATGAAAAATGAGTTACTAAAGCATTTTAAATAATACCTGCCTTGTACCATTTT  
TTAAATAGAAGTTACTTCAATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAA

## **FIGURE 102**

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPV  
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP  
GYFDNLANTLLVLKLNRRNRI SAIPPKMFKLPLQLHLELNRNKIKNVDGLTFQGLGALKSLKM  
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE  
FCQKLSLDELTFNHL SRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNE  
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ  
MKKLQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD  
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDNELLHDAEMENY AHLRAQG  
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGA  
MARLECAAVGHAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN  
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPKLNWTKDDSPLVVTER  
HFFAAGNQLLIIVDSVDSDAGKYTCMSNTLGTGRGNVRLSVIPTPTCDSPQMTAPSLDDD  
WATVGVVIAAVCCVVGTSVLVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLD  
RQDGYVSSSESGSHHGFVTSSGAGFFLPQHDSSTCHIDNSSEADVEAATDLFLCPFLGSTGP  
MYLKGNVYGSDFPFETYHTGCSPPDRTVLMHDHYEPSYIKKKECYPCSHPSEESCERSFSN  
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDA  
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEEHNICTFKQTLNRYRTPNFQS  
YDLDT

### **Signal sequence:**

amino acids 1-19

### **Transmembrane domain:**

amino acids 746-765

### **N-glycosylation site.**

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,  
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

### **Glycosaminoglycan attachment site.**

amino acids 826-830

### **Casein kinase II phosphorylation site.**

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,  
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,  
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,  
1013-1017, 1019-1023, 1021-1025

### **Tyrosine kinase phosphorylation site.**

amino acids 607-615

### **N-myristoylation site.**

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,  
612-618, 623-629, 714-720, 873-879

[illegible]

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAATG  
 AAGGATGCAGGACGCAGCTTTCTCCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC  
 GAAGCTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA  
 TAAACCCAGAGTTAGACCCGCGGGGGTGTGGTGTGTTCTGACATAAAATAAATAATCTTAAAGCAGCTGTTCCCTCC  
 CCACCCCAAAAAAAGGATGATTGGAATGAAGAACCAGGATTACAAAGAAAAAAGTATGTTCATTTTCTCT  
 TATAAAGGAGAAAGTGACCAAGGAGATATTTTTTGAATGAAAAAGTTTTGGGGCTTTTTTAGTAAAGTAAAGAACT  
 GGTGTGGTGGTGTTTTTCTTTCTTTTTGAATTTCCCAAGAGGAGAGGAAATTAATAATACATCTGCAAAGAAA  
 TTTTCTGAGAGAAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACCAGCAGAGCACAGTTGGA  
 TTTGTGCTTATGTTGACTAAAAATTGACGGATAATTGACAGTTGGATTTTTCTTTCATCAACCTCCTTTTTTTTTAAAT  
 TTTTATTCTCTTTGGTATCAAGATCATGCGTTTTCTCTGTTCTTAAACCCTGGATTTCCATCTGGATGTGTGCT  
 GTGATCAGTCTGAAATACAACCTGTTTGAATTCAGAAAGGACCAACACAGATAAAATTATGAATGTTGAACAAGAT  
 GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTTAAACAGGGCCCTATTTGACCCCCCTGCTTGTGGTGTCT  
 GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGCAGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA  
 CCAGTTTCAAGAGTGATTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGCGATCTCCACCAACACACAGCGCT  
 GCTGAACCTCCATGAGAAAAACCAATCCAGATCATCAAAGTGAAACAGCTTCAAGCACTTGAGGCACTTGGAAATCCT  
 ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGGCTTTCAATGGTCTGGCGAACCTCAACACTCTGGA  
 ACTCTTTGACAAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATACTTGTCTAAACTGAAGGAGCTCTGGTT  
 GCGAAACAACCCCATTTGAAAGCATCCCTTCTTATGCTTTTAAACAGAATTCCTTCTTTCGCGCCGACTAGACTTAGG  
 GGAATTTGAAAAGACTTTTACATACATCTCAGAAGGTGCCCTTTGAAGGTCTGTCCAACTTGAGGTATTTGAACCTTGC  
 CATGTGCAACCTTCCGGGAAATCCCTAACCCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA  
 TTTATCTGCCATCAGGCCCTGGCTCTTTCCAGGGTTTGTATGACACTTCAAAAACTGTGGATGATACAGTCCCAGAT  
 TCAAGTGATTGAACGGAATGCCTTTGTACAACTTTCAGTCACTAGTGAGAGATCAACCTGGCACAACAATCTGTAACT  
 ATTACTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGAGCGGATACATTTACATCACAAACCTTGGAACTG  
 TAACCTGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGTGCCCCGGTG  
 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTACATGCTATGCTCCGGT  
 GATTGTGGAGGCCCCCTGCAGACCTCAATGTCTCAATGAAGGCATGGCAGCTGAGCTGAAATGTGGGCCCTCCACATC  
 CCTGACATCTGTATCTTGGATTACTCCAAATGGAACAGTCACTGACATCTGGGGCGTACAAAGTGGCGGTATAGCTGT  
 GCTCAGTGATGGTACGTTAAATTTCAAAATGTAACCTGTGCAAGATACAGGCATGTACACATGTATGGTGTGAGTAA  
 TTCCGTTGGGAATACTACTGCTTTCAGCCACCCTGAATGTTACTGCAGCAACCACTACTCCTTTCTCTTACTTTTT  
 AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCACAGATAACAATGTGGGTCCCACCTCC  
 AGTGGTCGACTGGGAGACCACCAATGTGACCACCTCTCTCACACCAAGAGCACAAAGTTCGACAGAGAAAACTT  
 CACCATCTCCAGTGACATGATATAAACAGTGGGATCCAGGAATTGATGAGTTCATGAAGACTACCAAAATCATCAT  
 TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAAGTAGGGAAGCAGCACC  
 TCGGCAAAACCATCACGCCCCAACAAAGGACTGTTGAAATTATTAATGTGGATGATGAGATTACGGGAGACACACC  
 CATGGAAGCCACCTGCCCATGCCCTGCTATCGAGCATGAGCACCTAAATCACATATAACTCATACAAATCTCCCTT  
 CAACCACACAACAACAGTTTAAACACAATAAAATTCATACACAGTTTCAAGTGCATGAACCGTTATTGATCCGAATGAA  
 CTCTAAAGACAATGTACAAAGACACTCAAATCTAAACATTTACAGAGTTACAAAAAACAACCAATCAAAAAAAA  
 GACAGTTTTATTAATAAGACACAATGACTGGGCTAAATCTACTGTTTCAAAAAAGTGTCTTTACAAAAAACAA  
 AAAAGAAAAGAAATTTATTTATTAATAAATTCATTTGTGATCTAAAGCAGACAAAAA

## **FIGURE 104**

MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC  
VRKNLREVPDGI STNTRLLNLHENQIQI IKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA  
NLNTLELFDNRLTTIPNGAFVYLSKLLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS  
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKDELDSLGNHLSAIRPGSFQGLMHLQKL  
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNDIL  
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE  
LKCRASSTLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNVSGN  
TTASATLNVTAATTTFFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ  
STRSTEKTFTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN  
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHTTTVNTINSIHSS  
VHEPLLIRMNSKDNVQETQI

### **Signal sequence:**

amino acids 1-44

### **Transmembrane domain:**

amino acids 523-543

### **N-glycosylation site.**

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,  
442-446, 488-492, 606-610

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 183-187

### **Casein kinase II phosphorylation site.**

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

### **N-myristoylation site.**

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,  
391-397, 422-428, 433-439, 531-537

[illegible]

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCTTTTCGGTTTTCCCTCCTGCTGTTTTGGGGGCA  
TGAAAGGGCTTCGCCGCCGGGAGTAAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACGCGACCGC  
GAGGCGGGGCGTGACCCCTCGGCTGGAAGTTTGTGCCGGGCCCCGAGCGCGCGCCGGCTGGGAGCTTCGGGTTAGA  
GACCTAGGCCGCTGGACCGCGATGAGCGCGCCGAGCCCTCCGTGCGCGCGCCCGGGGTTGGGGCTGCTGCTGTGC  
GCGGTGTGGGGCGCGCTGGCCGGTCCGACAGCGCGCGTCCGCGGGAACTCGGGCAGCCCTCTGGGGTAGCCGCC  
GAGCGCCCATGCCCCACTACCTGCCGCTGCCCTGGGGACCTCGCTGGACTGCAATCGTAAGCGGCTAGCGCGCTCTT  
CCCCGAGCCACTCCCGTCTTGGGTGCTCGGCTGGACTTAAGTCACAACAGATTATCTTTTCATCAAGGCAAGTTCC  
ATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAACTGAACAACAATGAATTGGAGACCATTCCAAATCTGGGACCA  
GTCTCGGCAAATATTACACTTCTCTCTTGGCTGGAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG  
TTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTGCATTTCCAGCCCACAG  
CTCAAATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGCCCAACACA  
CTCCTTGTGTTAAAGCTGAAACAGGAACCGAATCTCAGCTATCCCACCCAAGATGTTTAAACTGCCCCAACTGCAA  
CATCTCGAATTGAACCGAAACAAGATTAAAAATGTAGATGGACTGACATTTCCAAGGCCTTGGTGCTCTGAAGTCT  
CTGAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTTTGGGGGCTGAGCAACATGGAATTTTG  
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTTACGGCTTGCTGATGCTGCAGGAACCTCAT  
CTCAGCCAAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA  
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTTGGCCTAAGCTTACTAAATACACTGCACATTTGGG  
AACAACAGAGTCAGCTACATTTGCTGATTGTGCCTTCCGGGGGCTTTCCAGTTTAAAGACTTTTGGATCTGAAGA  
AATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTC  
CAAGGAAATCGGATCCGTTCTATTACTAAAAAAGCCTTCACTGGTTTGGATGCATTGGAGCATCTAGACCTGAGT  
GACAACGCAATCATGCTTTTACAAGGCAATGCATTTTACAAATGAAGAACTGCAACAATTGCATTTAAATACA  
TCAAGCCTTTTGTGCGATTGCCAGCTAAAAATGGCTCCCACAGCTGGGTGGCGGAAAAACAACTTTCAGAGCTTTGTA  
AATGCCAGTTTGTGCCCATCTCAGCTGCTTAAAGGAAGAAGCATTTTGGCTGTTAGCCAGATGGCTTTGTGTGT  
GATGATTTTCCCAAACCCAGATCACGGTTGAGCCAGAAACAGTCGGCAATAAAAGGTTCCAATTTGAGTTTTC  
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTTGTGTTGGAAAAAGACAATGAACACTGTCATGAT  
GCTGAAATGGAAATTTATGCACACCTCCGGGCCCCAAGGTGGCGAGGTGATGGAGTATACCACCATCTTCCGCTC  
CGCGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCACTTCCAATCACTTTGGTTTCATCCTACTCTGT  
AAAGCCAAGCTTACAGTAATAATGCTTCCCTCATTTACCAACAGCCCCATGGATCTCACCATCCGAGCTGGGGCC  
ATGGCCAGCTTGGATGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGGGCACAGAC  
TTCCAGCTGCACGGGAGAGACGCTAGCTGTGATGCCCGAGGATGACGTGTTCTTTTCTCGTGGATGTGAAGATA  
GAGGACATTTGGGTATACAGCTGCACAGCTCAGAACAGTGCAAGGAAGTATTTTCAGCAAATGCAACTCTGACTGTC  
CTAGAAACACCATCATTTTTTGCGGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAAAACGCCGCTCCTACAGTGC  
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCAATTGGTGGTAAACCGAGAGGCAC  
TTTTTTGCGACGAGGCAATCAGCTTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAAATACACATGTGAG  
ATGCTTAACACCCCTTGGCACTGAGAGAGGAAACGTCGCCCTCAGTGTGATCCCCACTCAACCTGCGACATCCCC  
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGCTCGTGATCATAGCCGTGGTTTGTGT  
GTGGTGGGCACGTCACTCGTGTGGGTGGTCATCATATACCACACAAGGCGGAGGAATGAAGATTGCAGCATTAC  
AACACAGATGAGACCAACTTGCACAGCAGATATTCCTAGTTATTTGTCACTCAGGGAACGTTAGCTGACAGGCAG  
GATGGGTACGTGCTTTCAGAAAGTGAAGGCCACCACAGTTTGTACATCTTCAGGTGCTGGATTTTTTCTTACCA  
CAACATGACAGTAGTGGGACCTGCCATTTGACAATAGCAGTGAAAGCTGATGTGGAAGCTGCCACAGATCTGTTCT  
CTTTGTCGTTTGTGGGATCCACAGGCCCTATGTAATTTGAAGGAAATGTGATGCTCAGATCTCTTTTGAAACA  
TATCATACAGGTTGCAGTCTCTGACCCAAGAACAGTTTTAATGGACCACTATGAGCCCACTTACATAAAGAAAAAG  
GAGTGTACCCATGTTCTCATCCTTCAGAAGAATCCTGCGAACGGAGCTTCAGTAATATATCGTGGCCTTCACAT  
GTGAGGAAGCTACTTAACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAAATCTGTGTCTAAACAAGTCC  
TCTTTAGATTTTAGTGCAAAATCCAGAGCCAGCGTGGTTGGCTCGAGTAATCTTTTCATGGGTACCTTTTGGAAAA  
GCTCTCAGGAGACCTCACCAGATGCTTATTCAAGCTTTGGACAGCCATCAGATTGTGAGCCAAAGAGCCTTTTAT  
TTGAAAGCTCATTTCTTCCAGACTTGACACTCTGGGTGAGGAAAGATGGGAAGAAAGACAGATTTTCAGGAA  
GAAATACATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGTCTTATGACTTTTGAC  
ACATAGACTGAAATGAGACCAAAGGAAAAAGCTTAACATACTACCTCAAGTGAACCTTTTATTTAAAAAGAGAGAGAAT  
CTIATGTTTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAATGCTTTATTTATACAGATGAACCAAATTAC  
AAAAAGTTATGAAAAATTTTTATCTGGGAATGATGCTCATATAAGAATACCTTTTAAACTATTTTTTAACTTTG  
TTTTATGTCAAAAAGATCTTACGTAATTAATGATATAAAATCATGATTTATTTATGATTTTTTATAATGCCAGA  
TTCTTTTATGGAATAAGTACTACTAAAGCAATTTAAATAAATACTGCCCTGTACCACTTTTATAATAGAAGTT  
ACTTCATTATATTTTGCACATTATATTTAATAAAATGTGTCAATTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

## **FIGURE 106**

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAAERPCPTTCRCLGDLDDCSR  
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT  
LLSLAGNRIVEILPEHLKEFQSLETDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY  
FDNLANTLLVLKLNRRNRI SAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR  
NGVTKLMDGAFWGLSNMEILQLDHNRLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC  
QKLSELDLTFNHL SRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSSLKTLDLKNNEIS  
WTIEDMNGAFSGLDKLRRLLIQGNRIRSITKKAFTGLDALEHLDSLDAIMSLQGNAFSQMK  
KLQQLHLNTSSLLCDCQLKWL PQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDF  
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENY AHLRAQGGE  
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA  
RLECAAVGH PAPQIAWQKDG GTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA  
GSISANATLTVLETSPFLRPLLDRTVTKGETAVLQCIAGGSPPPKNLWTKDDSPLVVTERHF  
FAAGNQLLIIVDSVDAGKYTCEMSNTLGTGRGNVRLSVIPTPTCDSPQMTAPSLDDDGWA  
TVGVVIIAVVCCVVGTSVLVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGT LADRQ  
DGYVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY  
LKG NVYGS DPFETYHTGCSPDPRTV LMDHYEPSYIKKKECYPCSHPSEESCERSFSNISWPS  
HVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTFGKALRRPHLDAYS  
SFGQPSDCQPRAFYLKAHSSPDLD SGSEEDGKERTDFQEENHICTFKQTL ENYRTPNFQSYDLDT

**Signal sequence:**

amino acids 1-27

**Transmembrane domain:**

amino acids 808-828

**N-glycosylation site.**

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,  
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

**Glycosaminoglycan attachment site.**

amino acids 886-890

**Casein kinase II phosphorylation site.**

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,  
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,  
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,  
1073-1077, 1079-1083, 1081-1085

**Tyrosine kinase phosphorylation site.**

amino acids 667-675

**N-myristoylation site.**

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,  
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

**Leucine zipper pattern.**

amino acids 58-80, 65-87

## FIGURE 107

CAAAACTTGCCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC  
TGGGGGAGCGCGTTTCGGCCTGTGGGGCGCCGCTCGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC  
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCCCCTGGGTGGTCCCGTCCCCATCCCTCCTTTATATA  
GAAACCTTCCACACTGGGAAGGCAGCGGCGAGGCAGGAGGGCTCATGGTGAGCAAGGAGGCCGGCTGATCTGCAG  
GCGCACAGCATTCCGAGTTTACAGATTTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCCTGGT  
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCCAGAGCCGGGTGCTGC  
TGCTCCTGCTGCTGCTGCCGCCACAGCTGCACCTGGGACCTGTGCTTGCCGTGAGGGCCCCAGGATTTGGCCGAA  
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTTGCGGAGGAGGAGCCGGTGCTGGTACTGAGCCCTGAGG  
AGCCCCGGGCTGGCCCAGCCGCGGTGAGCTGCCCCCGAGACTGTGCCTGTTCCCAGGAGGGCGTCTGGACTGTG  
GCGGTATTGACCTGCGTGAGTTCCCGGGGACCTGCCTGAGCACACCAACCACCTATCTCTGCAGAACAAACCAGC  
TGGAAAAGATCTACCTGAGGAGCTCTCCCGGCTGCACCGGCTGGAGACACTGAACCTGCAAAACAACCGCCTGA  
CTTCCCGAGGGCTCCCAGAGAAGGCGTTTGGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAATAACAAGC  
TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAGATCT  
ATGGGCTCACCTTTGGCCAGAAGCCAAACTTGAGGTCTGTGTACCTGCACAACAACAAGCTGGCAGACGCCGGGC  
TGCCGACAAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCTGTCCAGCAACTTCTGCGCCACGTGC  
CCAAGCACCTGCCGCTGCCCTGTACAAGCTGCACCTCAAGAACAACAAGCTGGAGAAGATCCCCCGGGGGCCT  
TCAGCGAGCTGAGCAGCCTGCGCGAGCTATACCTGCAGAACAACTACCTGACTGACGAGGGCCTGGACAACGAGA  
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGGCTGC  
CGCGCAGCCTGGTGCTGCTGCACCTTGGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC  
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCCAGGGCC  
TCAAGCGTGTGCACACGGTGCACCTGTACAACAACGCGCTGGAGCGCGTGCACAGTGGCCTGCCTCGCCGCGTGC  
GCACCTCATGATCCTGCACAACCAGATCACAGGCATTGGCCGCGAAGACTTTGCCACCACCTACTTCTGGAGG  
AGCTCAACCTCAGTACAACCGCATCACCAGCCACAGGTGCACCGGACGCTTCCGCAAGCTGCGCCTGCTGC  
GCTCGCTGGACCTGTGCGGCAACCGGCTGCACACGCTGCCACCTGGGCTGCCTCGAAATGTCCATGTGCTGAAGG  
TCAAGCGCAATGAGCTGGCTGCCTTGGCACGAGGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA  
CCAGCAACCGACTGCGCAGCCGAGCCCTGGGCCCCCGTGCCTGGGTGGACCTCGCCCATCTGCAGCTGCTGGACA  
TCGCCGGGAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCACTTGAGTACCTGTACCTGCAGAACAA  
AGATTAGTGCGGTGCCCGCCAATGCCTTCGACTCCACGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAAACAAGC  
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTTCCGGAGGCTGAAGCACCTGCAGGTCTTGGACATTGAAGGCAACT  
TAGAGTTTGGTGACATTTCCAAGGACCGTGGCCGCTTGGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG  
AGGAAGAGGAAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGGACTCTTTTCTGC  
AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACACCCAGCTGCACACATGAGGCA  
TCCCACATGACACGGGCTGACACAGTCTCATATCCCCACCCCTTCCCACGGCGTGTCCCACGGCCAGACACATGC  
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACCTACCCTCCAAACCACCACAGTCTCTGTACAC  
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAAGGGTCTGCCCCCTGCCCTGGCACACACAGGCACCCA  
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACACACACATGCACAAGTCATGTGCGAA  
CAGCCCTCCAAAGCCTATGCCACAGACAGCTCTTGCCCCAGCCAGAATCAGCCATAGCAGCTCGCCGTCTGCCCT  
GTCCATCTGTCCGTCCGTTCCTGGAGAAGACACAAGGGTATCCATGCTCTGTGGCCAGGTGCCTGCCACCCTCT  
GGAACCTCAAAAAGCTGGCTTTTATTTCCCTTCCCATCCTATGGGGACAGGAGCCTTCAGGACTGCTGGCCTGGCC  
TGGCCACCCCTGCTCCTCCAGGTGCTGGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA  
CAGGCACTTTTCCAATGGGCAAGCCAGTGGAGGCAGGATGGGAGAGCCCCCTGGGTGCTGCTGGGGCCTTGGGG  
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTTT  
GTTCTTCAGGCCGTGGGGGAAGTTCCGGGTGCCTTTATTTTTTATTCTTTTCTAAGGAAAAAATGATAAAAAT  
CTCAAAGCTGATTTTCTTGTATAGAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAA

## **FIGURE 108**

MEGEEAEQPAWFHQWRPGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPVLAVRAPGFGRS  
GGHSLSPREENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVDCGGIDLREFPGDLP  
EHTNHLSQLNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK  
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV  
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN  
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLTPIRSLEYLLLHSN  
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMLHNQITGIGREDFATTYF  
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA  
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL  
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD  
RGRLGKEKEEEEEEEEEEEEEETR

### **Signal sequence:**

amino acids 1-48

### **N-glycosylation site.**

amino acids 243-247, 310-314, 328-332, 439-443

### **Casein kinase II phosphorylation site.**

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

### **N-myristoylation site.**

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,  
477-483, 498-502, 539-545, 548-554

### **Leucine zipper pattern.**

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,  
535-557

## FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCCTCCGGGAGCGGCAG  
CAGTAGCCCCGGGCGGCGAGGGCTGGGGGTTCCTCGAGACTCTCAGAGGGGCGCCTCCCATCGGCGCCCACCACCC  
CAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCCAACATGGATTTCCTGGCGCTGGT  
GCTGGTATCCTCGCTCTACCTGCAGGCGGCCGCCGAGTTTCGACGGGAGGTGGCCAGGCAAATAGTGTATCGAT  
TGGCCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTGAGCC  
TGTGTGCCAACCACGATGCAAAATGTTGTAATGTATCGGGCCAAACAAGTGCAAGTGTATCCTGGTTATGCTGG  
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTA  
CGGCAGCTACAAGTGTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTTCCTGCTCAAGTGCCCTGACCTG  
CTCCATGGCAAACTGTCAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCTGGCCT  
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATT  
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCTATAAAGGCTTCGATCTCATGTATATTGGAGG  
CAAATATCAATGTCTATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGACAGCAGCTTTGCTCGATGTTATAA  
CGTACGTGGGTCTTACAAGTGCAAAATGTAAAGAAGGATACAGGGTGATGGACTGACTTGTGTGTATATCCCAA  
AGTTATGATTGAACCTTCAGGTCCAATTTCATGTACCAAAGGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA  
TAATAATTGGATTCTCTGATGTTGGAGTACTTGGTGGCCTCCGAAGACACCATATATTCCTCCTATCATTACCAA  
CAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAAGCCAACACCAATTCCTACTCCACCACCACCACCACC  
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACCCAGGACTGACAACCTATAGC  
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAAACAGGGTACAGACAGACCCCTCAGAAACCCAGAGG  
AGATGTGTTTCAGTGTCTGGTACACAGTTGTAATTTTGACCATTGGACTTTGTGGATGGATCAGGGAGAAAGACAA  
TGACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTCCGCAGCCAAAGCCCCAGG  
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCTCATGCATTTCAGGGGACCTGTGCCTGTCTATTTCAGGCA  
CAAGGTGACGGGGCTGCACCTCTGGCACACTCCAGGTGTTTGTGAGAAAAACGGTGCCACGGAGCAGCCCTGTG  
GGGAAGAAATGGTGGCCATGGCTGGAGGCAAAACAGATCACCTTGCAGGGGGCTGACATCAAGAGCGAATCACA  
AAGATGATTTAAAGGGTTGGAAAAAAGATCTATGATGGAAAAATTAAGGAACTGGGATTATTGAGCCTGGGAGAG  
AGAAGACTGAGGGGCAAACCATGATGGTTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTG  
TTCTCCATATGCACCTAAGAATAGAACAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTTCCTGGCAGG  
GGCCATTGTTAGAATACTTCATAAAAAAAGAGTGTGAAAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGA  
TAAAAATTTGCTATTTTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAAGTAACAAATTATAGAATTTCCCAA  
AGATGTTTTGATCCTACTAGTAGTATGCAGTGAAAACTTTTGAACATAAATAATTTGGACAAGGCTTAATTTAGG  
CATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCACCAAATGCTGAGCTCACTGAAATA  
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGAC  
AGATATTTTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC  
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAAGAGATCCTTCAAGGAACACAGTTTCAGAGAG  
ATTTTCATCGGGTGCAATCTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGCCCTGCCCC  
ACACCGGCAGACCTTTCCCTTCACCTCATCAGTATGATTGAGTTTCTCTTATCAATTGGACTCTCCAGGTTCAC  
AGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGGTCTTCTGTGTCATTTAACCTGGTAAAGGCAGGGCTGG  
AGGGGGAAAAATAAATCATTAAGCCTTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTTTAAATGGTTTCATT  
TCCTTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGGAAAAATAAATGAAAAATTTTACTTTTCGATGCCAA  
TGATACATTGCACATAAATGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTTGTATTATTTAATGTTTTT  
CTAAAAATAAAAAATGTTAGTGGTTTTCCAAATGGCCTAATAAAAAACAATTATTTGTAAATAAAAAACACTGTTAGTAAT

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCCTCCGGGAGCGGCAG

## **FIGURE 110**

MDFLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP  
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD  
GSCSSALTCSMANCQYGC DVVKQI RCQCPS PGLHLAPDGR TCVDVDECATGRASCPRFRQC  
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDEC SLGQYQC SSFARCYNVRGSYKCKCKEGYQG  
DGLTCVYIPKVMIEPSGPIHV PKNGTILK GDTGN NNWIPDVGSTWWPPKTPYIPPIITNRP  
TSKPTTRPTPKPTPIPTPPPPPLPT ELRTPLPPTT PERPTTGLTTIAPA ASTPPGGITVDN  
RVQTD PQKPRGDVFSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTV SAAKAPGG  
KAARLVLP LGR LMHSGDLCL SFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI  
TLRGADIKSESQR

### **Signal sequence:**

amino acids 1-17

### **N-glycosylation site.**

amino acids 273-277

### **Casein kinase II phosphorylation site.**

amino acids 166-170, 345-349

### **Tyrosine kinase phosphorylation site.**

amino acids 199-206

### **N-myristoylation site.**

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,  
421-427, 433-439, 462-468, 476-482

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

### **Cell attachment sequence.**

amino acids 382-385

### **EGF-like domain cysteine pattern signature.**

amino acids 75-87

## FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCCTTTAGATTGTGA  
AATGTGGCTCAAGGTCTTCACAACCTTTCCTTTCCTTTGCAACAGGTGCTTGCTCGGGGCTGA  
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC  
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA  
CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGAATACC  
AACACAAGTTCACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCTT  
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTCTATCTGCCAGTCA  
GAAGATACAAGTCACGGTTGATGATCCTGTCACAAAGCCAGTGGTGCAGATTCATCCTCCCT  
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG  
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC  
TCCCCAAAACAATACCCTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT  
GCCTGGTGAGGAACCCTGTCAGTGAAATGGAAAGTGATATCATTATGCCCATCATATATTAT  
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT  
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT  
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGGCCTCGCTTAGAAGTT  
GCATCTGAGAAAGTAGCCCAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC  
CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG  
CACAGAAAGGAAAATCATTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTTTGATT  
ATATCCATGTGTCTTCTCTTCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAA  
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG  
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTTCCAGG  
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGGCAAGATTTGCACAGTACAGT  
GTATGAAGTTATTTCAGCACATCCCTGCCCAGCAGCAAGACCATCCAGAGTGAACCTTTCATGG  
GCTAAACAGTACATTTCAGTGAAATTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAGT  
ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA  
TGCAGAATAGAGGCATTTATGCAAATTGAACTGCAGGTTTTTTCAGCATATACACAATGTCTT  
GTGCAACAGAAAAACATGTTGGGGAAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG  
GGAGAACGAAAGTGACAGGGGTTTCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA  
ATTAGTTCTACTCTACACTTTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA  
TGTGGAAACTTTTACATTGTTTCGATTTTTTCAGCAGACTTTGTTTTATTAAATTTTTATTAGTG  
TTAAGAATGCTAAATTTATGTTTTCAATTTTATTTCCAAATTTCTATCTTGTTATTTGTACAA  
CAAAGTAATAAGGATGGTTGTACAAAAACAAAACCTATGCCTTCTCTTTTTTTTCAATCACC  
AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA  
TTTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTTGCTTTTAAAAAAAAAAAAAA

## **FIGURE 112**

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVVRGQALYLPVHYGFHTPASDIQIIWLFERPH  
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQ  
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS  
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV  
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT  
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK  
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV  
YEVIQHIPAQQQDHPE

### **Signal sequence:**

amino acids 1-18

### **Transmembrane domain:**

amino acids 341-359

### **N-glycosylation site.**

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,  
276-280, 308-312

### **Casein kinase II phosphorylation site.**

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

### **Tyrosine kinase phosphorylation site.**

amino acids 272-280

### **N-myristoylation site.**

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,  
239-245

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 7-18

## FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGACAGTTCCCCTGGCAGTCCTGGTGCTGTT  
GCTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGA  
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCT  
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAA  
TATTGCGAAAGTAGATGTACAGAGCAGCCAGGACTGAGTGGACGGTTTTATCATAACTGCTC  
TTCCTACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG  
AAGGACTTCATAAAC'TTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTTATCATG  
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA  
TCAGGACGTGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACT  
GTTTTTGTCTTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC  
AGATTGCC'TTTGTCTTCAAAAAGGCGCAGACCACAGCCATAACCATAACCCTTCAAAAAAAT  
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGAGGAGGAACAAGAGGCGGATGAAGAA  
GATGTTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCCACAGAATGC  
CATAAGACAACGCTCTCTGGGTCCATCATTGGCCACAGATAAAATCCTAGTTAAATTTTATAG  
TTATCTTAATATTATGATTTTGATAAAAACAGAAGATTGATCATTTTGT'TTGGTTTGAAGTG  
AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCA'TTAAATTGAAGAGTCTA  
CATTCAGAACATAAAAGCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATG  
GTTTAAATAGTTCTCTAATTTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT  
TTAATAATAACCTATTTCAAGTCTGAGTTTTTGA'AATTTACATTTCCCAAGTATTGCATTAT  
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTTCTCTG  
TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG  
AAATGTGTATTTCAGTGACAATTTCTGTTCTTTTTAGAGGTATATTCCAAAATTTCTTGT  
ATTTTTAGGTTATGCAACTAATAAAAACCTTACATTAATTAATTACAGTTTTCTACACA  
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTC  
CAACAAAGTTTGATTTTCTCTTGATTTTTCTTACTTACTATGGGTACATTTTTTATTTTT  
CAAATTGGATGATAATTTCTTGAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTT  
GTTTCAAAC'TGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAATTT  
TTGGCCACTTTTTTCAGATTTTACATCATTCTTGCTGAAC'TTCAACTTGAAATTGTTTTTTT  
TTTCTTTTTGGATGTGAAGGTGAACATTCCTGATTTTTTGTCTGATGTGAAAAAGCCTTGGA  
TTTTACATTTTTGAAAATTCAAAGAAGCTTAATATAAAAGTTTGCATTCTACTCAGGAAAAAG  
CATCTTCTTGATATATGTCTTAAATGTATTTTTTGTCTCATATACAGAAAGTTCTTAATTGAT  
TTTACAGTCTGTAATGCTTGATGTTTTTAAATAATAACATTTTTTATATTTTTTAAAGACAA  
ACTTCATATTATCCTGTGTTCTTTCTGACTGGTAATATTGTGTGGGATTTACAGGTAAAA  
GTCAGTAGGATGGAACATTTTAGTGTATTTTTACTCCTTAAAGAGCTAGAATACATAGTTTT  
CACCTTAAAGAAGGGGGAAAATCATAAATACAATGAATCAACTGACCATTACGTAGTAGAC  
AATTTCTGTAATGTCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG  
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTTGTACCATT  
AAAGAGTTTGGATGTGTAACCTTGATGCCTTAGAAAAATATCCTAAGCACAAAATAAACCT  
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAAAAA

[illegible]

Signal sequence:

**Transmembrane domain:**

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

[illegible]

CGAGTGTCCAGACTGCGGAGACCCGTTAGATAATTCGTTAACTAATTCAACAAACGGGACCCCTT  
CTGTGTGCCAGAAACCGCAAGCAGTGTGCTAATCCAGTGGGACAGGCGGATTGGAAGAGCGGG  
AAGGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC  
ATTGCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCCTTACCTCTATTG  
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC  
CTTGTGGAGGAAGCCAAGCTTTCCAAGATTAAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC  
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG  
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTCTGCAGGACTCAGCTGCA  
GGTTTTATCGCCAACCTCTCTGTGAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGG  
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA  
GAGGGGAACTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG  
GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTGTGATGAGACAGGTGCT  
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA  
GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTACCCGCCGCCTGCTC  
TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA  
GGAAGAGAGAGAAAAAACGTTAAACAAATCAGACAGAAGCTGAGCTAGCAACCCCAGAAGGCA  
TCTATGAGAGGCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTGG  
GAGGGTGTCAAAC TGACACCCGTAGACAGAAGAGGCTTTTTCTGTAGGTACCACCATGGCAA  
CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA  
TCGT CAGGTACTACGATGT CATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGAAAA  
CCTAAACTTGCACGAGCCACCGTTCGTGATCCCAAGACAGGAGTCCTCACTGTCGCCAGCTA  
CCGGGTTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAAT  
GTCGGATGCAGCATATCACAGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAT  
TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCG  
CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTTCTTAACTACATGAGTGATGTAGAAGCTG  
GTGGTGCCACCGTCTTCCCTGATCTGGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG  
TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAAGACATGCTGCCTGCC  
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT  
TGAGACCTTGTGGATCAACAGAAGTTGACTTGACATCCTTTTCTGTCTTCCCTTCCCTGGT  
CTTCAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCCCTTGTATGTTCCCTATCAGGCT  
GATTTTTTGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT  
GTGACTGAAGTCCCAGCCCTTCCATT CAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA  
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT  
TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTTGTTTACATGTTTGTTTTTAT  
GGCATTCTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

## **FIGURE 116**

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA  
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFP  
TDEDEIGAALKMRLQDTYRLDPGTISRGLPGTKYQAMLSVDDCFGMGRSAYNEGDIYHTV  
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR  
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVDYLPERDVYESLCRGEGVKLTPRRQKRLF  
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYDVMSEIEIERIKEIAKPKLARATVRDPKTG  
VLTVASYRVSKSSWLEEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS  
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGECDYR  
TRHAACPVLVGCKWVSNKWFHERGQEFRLPCGSTVD

**Signal sequence:**

amino acids 1-17

**N-glycosylation site.**

amino acids 115-119, 264-268

**Glycosaminoglycan attachment site.**

amino acids 490-494

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 477-481

**Casein kinase II phosphorylation site.**

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,  
346-350, 365-369, 385-389, 457-461, 530-534

**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

**N-myristoylation site.**

amino acids 14-20, 131-137, 171-177, 446-452

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 8-19

**Leucine zipper pattern.**

amino acids 213-235

Species	Sex	Age	Length	Wing	Tail	Culmen	Tarsus	Middle toe	Claw	Weight
<i>Actitis macularia</i>	♂	Ad.	180	110	100	25	100	35	15	1000
<i>Actitis macularia</i>	♀	Ad.	170	105	95	25	95	35	15	900
<i>Actitis macularia</i>	♂	Ad.	175	108	98	25	98	35	15	950
<i>Actitis macularia</i>	♀	Ad.	165	102	92	25	92	35	15	850
<i>Actitis macularia</i>	♂	Ad.	185	115	105	25	105	35	15	1100
<i>Actitis macularia</i>	♀	Ad.	175	108	98	25	98	35	15	1000
<i>Actitis macularia</i>	♂	Ad.	180	110	100	25	100	35	15	1050
<i>Actitis macularia</i>	♀	Ad.	170	105	95	25	95	35	15	950
<i>Actitis macularia</i>	♂	Ad.	185	115	105	25	105	35	15	1150
<i>Actitis macularia</i>	♀	Ad.	175	108	98	25	98	35	15	1050
<i>Actitis macularia</i>	♂	Ad.	180	110	100	25	100	35	15	1100
<i>Actitis macularia</i>	♀	Ad.	170	105	95	25	95	35	15	1000
<i>Actitis macularia</i>	♂	Ad.	185	115	105	25	105	35	15	1150
<i>Actitis macularia</i>	♀	Ad.	175	108	98	25	98	35	15	1050
<i>Actitis macularia</i>	♂	Ad.	180	110	100	25	100	35	15	1100
<i>Actitis macularia</i>	♀	Ad.	170	105	95	25	95	35	15	1000
<i>Actitis macularia</i>	♂	Ad.	185	115	105	25	105	35	15	1150
<i>Actitis macularia</i>	♀	Ad.	175	108	98	25	98	35	15	1050
<i>Actitis macularia</i>	♂	Ad.	180	110	100	25	100	35	15	1100
<i>Actitis macularia</i>	♀	Ad.	170	105	95	25	95	35	15	1000
<i>Actitis macularia</i>	♂	Ad.	185	115	105	25	105	35	15	1150
<i>Actitis macularia</i>	♀	Ad.	175	108	98	25	98	35	15	1050
<i>Actitis macularia</i>	♂	Ad.	180	110	100	25	100	35	15	1100
<i>Actitis macularia</i>	♀	Ad.	170	105	95	25	95	35	15	1000
<i>Actitis macularia</i>	♂	Ad.	185	115	105	25	105	35	15	1150
<i>Actitis macularia</i>	♀	Ad.	175	108	98	25	98	35	15	1050
<i>Actitis macularia</i>	♂	Ad.	180	110	100	25	100	35	15	1100
<i>Actitis macularia</i>	♀	Ad.	170	105	95	25	95	35	15	1000
<i>Actitis macularia</i>	♂	Ad.	185	115	105	25	105	35	15	1150
<i>Actitis macularia</i>	♀	Ad.	175	108	98	25	98	35	15	1050
<i>Actitis macularia</i>	♂	Ad.	180	110	100	25	100	35	15	1100
<i>Actitis macularia</i>	♀	Ad.	170	105	95	25	95	35	15	1000
<i>Actitis macularia</i>	♂	Ad.	185	115	105	25	105	35	15	1150
<i>Actitis macularia</i>	♀	Ad.	175	108	98	25	98	35	15	1050
<i>Actitis macularia</i>	♂	Ad.	180	110	100	25	100	35	15	1100
<i>Actitis macularia</i>	♀	Ad.	170	105	95	25	95	35	15	1000
<i>Actitis macularia</i>	♂	Ad.	185	115	105	25	105	35	15	1150
<i>Actitis macularia</i>	♀	Ad.	175	108	98	25	98	35	15	

CAGCATATTGATTTTTACTTCTCTCTCTTTTCTAGTGAAGACAGACCATAATCCCAGTGTGAGTGAAATTGATTGT  
 TTCAITTTTATTACCGTTTGGCTGGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA  
 AGACAGGACAATCTTCTTGGGGATGCTGGTCTCTGGAAGCCAGCGGGCTTGCTCTGTCTTTGGCCTCATTGACCC  
 CAGGTTCTCTGGTTAAACTGAAAGCCTACTACTGGCCTGGTGCCCATCAATCCATTGATCCTTGAGGCTGTGCC  
 CCTGGGGCACCCACCTTGGCAGGGCCTACCACTGCGACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC  
 CCCTCATCTTAGGGCTGTCTCTGGGGTGACAGCTGAGCCTCAGTCCGGGTTTCTGGATCCAGGGGAGGGGAAG  
 ATCCCTGTGTCTGAGGCTGTAGGGGAGCGAGGAGGGCCACCAATCCAGATTCTCAGAGCTCGGCTAGACCAAAAGT  
 ATGAAGACTTCAAACCCGGATGTGTCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC  
 GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTTGACCTCCCGAGCTACACTGTCCA  
 CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCACTGGGCAGCGGGGG  
 CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGGATGAGCGGCCCGCCTGGCTCATGTCCAGAACCTTGC  
 GCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTTCATCATCAGGATGACACATATGTGCAGGCC  
 CCCGCTTGGCAGCCCTTGCTGGCCACTCTCAGCATCAACCAAGACTGTACTTAGCCCGGGCAGGAGGTTCTATTG  
 GCGCAGGCGAGCAGGCCCGGTATGCTCATGGGGCTTTTGGCTACCTGTTGTACGGAGTCTCCTGCTTCGTCCTGC  
 GGCCACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCCGTCTTGACGAGTGGCTTGGACGCTGCCTCATTG  
 ACTCTCTGGGCGTCGGCTGTGTCTCACAGCACCAGGGGCAGCAGTATCGCTCATTTGAACTGGCCAAAAATAGGG  
 ACCCTGAGAAGGAAGGGAGCTCGGCTTTCTTGAGTGCCCTTCGCCGTGCACCCGTGTCTCCGAAGGTACCCTCATGT  
 ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAATAAGAACAACTGCAGGCTCAGA  
 TCCGGAACTGACCGTGTCTGACCCCGAAGGGGAGCGAGGCTGAGCTGGCCCGTTGGGCTCCCTGCTCCTTTTCA  
 CACCACACTCTCGCTTTTGAGGTGCTGGGCTGGGACTACTTCAACAGAGCAGCACACCTTCTCCTGTGCAGATGGGG  
 CTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA  
 ATCGGCGCTATCAGCCCCGCTTGCCTTCCAGAAGCAGCGACTGCTCAACGGCTATCGGCGCTTCGACCCAGCAC  
 GGGGCATGGAGTACACCCCTGGACCTGCTGTTGGAATGTGTGACACAGCGTGGGCACCGCGGGGCCCTGGCTCGCA  
 GGGTCAGCCTGCTGCGGCCACTGAGCGAGGTGGAATCTACCTATGCCCTATGTCTACTGAGGCCACCCAGTGC  
 AGCTGTGTCTGCCACTCTCTGGTGGCTGAGCTGAGCGCCCGGCTTTCTCGAGGCGTTTGACGCCAATGTCTC  
 TGGAGCCACGAGAACAATGCATTGTCTACCCCTGTTGCTGGTCTACGGGCCACGAGAAGGTGGCCGTGGAGCTCCAG  
 ACCCATTTCTTGGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCCTGGGACGAGGCTGGCCCTGGCTCG  
 CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTCGAAGAAGCACCCCTGTGGACACTCTCT  
 TCTTCTTTACCACCGTGTGGACAAGGCCTGGGCCCGAAGTCTCAACCGCTGTGCGATGAATGCCATCTCTGGCT  
 GGCAGGCCCTCTTTCCAGTCCATTTCCAGGAGTTCAATCTGCCCTGTCAACACAGAGATCACCCCGAGGGCCCC  
 CGGGGGCTGGCCCTGACCCCCCTTCCCTCTGTTGCTGACCCCTCCCGGGGGCTCCTATAGGGGGGAGATTTG  
 ACCGGCAGGCTTCTGCGGAGGGCTGCTTCTACAACGCTGACTACCTGGCGGGCCGAGCCCGGCTGGCAGGTGAAC  
 TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTTCTCCGGTTCTCAGGGCTCC  
 ACCTCTTTTCGGGCGTAGAGCCAGGGCTGGTGCAGAAGTTCTCCCTGCGAGACTGCAGCCACGGCTCAGTGAAG  
 AACTCTACCACCGCTGCCGCCCTCAGCAACCTGGAGGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTCTTTG  
 AGCAGGAGCAGGCCAATAGCACTTAGCCCCCTGGGGGCCCTAACCTCATTACCTTTCTTTGTCTGCTGCAGCC  
 CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTTTAAATATGAAAATGTTATTAA  
 ACATGTCTTCTGCC

## **FIGURE 118**

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPD SRARLD  
QSD E D F K P R I V P Y Y R D P N K P Y K K V L R T R Y I Q T E L G S R E R L L V A V L T S R A T L S T L A V A V N R T V  
A H H F P R L L Y F T G Q R G A R A P A G M Q V V S H G D E R P A W L M S E T L R H L H T H F G A D Y D W F F I M Q D D T Y  
V Q A P R L A A L A G H L S I N Q D L Y L G R A E E F I G A G E Q A R Y C H G G F G Y L L S R S L L L R L R P H L D G C R G  
D I L S A R P D E W L G R C L I D S L G V G C V S Q H Q G Q Q Y R S F E L A K N R D P E K E G S S A F L S A F A V H P V S E  
G T L M Y R L H K R F S A L E L E R A Y S E I E Q L Q A Q I R N L T V L T P E G E A G L S W P V G L P A P F T P H S R F E V  
L G W D Y F T E Q H T F S C A D G A P K C P L Q G A S R A D V G D A L E T A L E Q L N R R Y Q P R L R F Q K Q R L L N G Y R  
R F D P A R G M E Y T L D L L L E C V T Q R G H R R A L A R R V S L L R P L S R V E I L P M P Y V T E A T R V Q L V L P L L  
V A E A A A P A F L E A F A A N V L E P R E H A L L T L L L V Y G P R E G G R G A P D P F L G V K A A A A E L E R R Y P G  
T R L A W L A V R A E A P S Q V R L M D V V S K K H P V D T L F F L T T V W T R P G P E V L N R C R M N A I S G W Q A F F P  
V H F Q E F N P A L S P Q R S P P G P P G A G P D P P S P P G A D P S R G A P I G G R F D R Q A S A E G C F Y N A D Y L A A  
R A R L A G E L A G Q E E E E A L E G L E V M D V F L R F S G L H L F R A V E P G L V Q K F S L R D C S P R L S E E L Y H R  
C R L S N L E G L G G R A Q L A M A L F E Q E Q A N S T

### **Signal sequence:**

amino acids 1-15

### **Transmembrane domain:**

amino acids 489-507

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-678

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250

## FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC  
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG  
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA  
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA  
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTGAGTATACTGTATTATCCTTGTAACC  
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG  
AGTTCCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTAATATGGACACAAATGACATG  
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACTG  
GTTCTTCCTTGACGCCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTTGTAA  
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT  
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT  
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC  
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA  
AAAGATGTATTTAATACCAAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC  
CAACCAGGTAGTAGAAGGCTGTTGTTGAGATATGGCTGTTACTTTTAATGGACTGACTCCAA  
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTGTTGGGCATATTTCAAT  
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG  
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACATACATATCCAA  
TACAGCTGTATGTTTCTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG  
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTTCTTTAAACACATGAACATTGTAAATG  
TGTTGGAAAGAAGTGTTTTAAGAATAATAATTTTGCAAATAAACTATTAATAAATATTATAT  
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTCTGATTGGTT  
AAAAAATTTTAACAGGTCTTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT  
TGTGATTAAAGTAAAACCTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT  
AAGCCTCCCAAGTTCCAATGGATTTGCCTTCTCAAATGTACAACCTAAGCAACTAAAGAAA  
ATTAAAGTGAAAGTTGAAAAAT

## **FIGURE 120**

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME  
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK  
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG  
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT  
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL  
PPNGSDND

### **Signal sequence:**

amino acids 1-33

### **N-glycosylation site.**

amino acids 121-125, 342-346

### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 319-323, 464-468

### **Casein kinase II phosphorylation site.**

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,  
399-403, 409-413, 473-477, 729-733, 748-752

### **Tyrosine kinase phosphorylation site.**

amino acids 736-743

### **N-myristoylation site.**

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,  
558-564, 651-657, 657-663, 672-672

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 14-25

### **Cell attachment sequence.**

amino acids 247-250

## **FIGURE 121**

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG  
AAAAAGAGAGAGAGAGAGAAACAAAAAACCAAAGAGAGAGAGAAAAAATGAATTCATCTAAATCAT  
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT  
GGGATCCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT  
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT  
ACAATTATGGATCAGGTTCAAGTCAAGAAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC  
AGCTGCTACTTCTTTTCTACTGACACCATTTCCTGGGCGTTAAGTTTAAAGAACTGCTCAGC  
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA  
AACCTAAAATGAGAGAGTTTTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGGTCAGTGGCAA  
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA  
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGCAAAATTGGA  
ATGATGTAACCTGTTTCCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTG  
AACAAAGGAAAATCTCTTTAAGAAACAGAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA  
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC  
ATAAGTATTTGTTACTCTGATACAAATAAAAAATAAGTAGTTTTAAATGTTAAAAAAAAAAAAA  
AAA  
AAAAA

## **FIGURE 122**

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN  
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ  
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPNNIATLEDCAIMRDSS  
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

### **Signal sequence:**

amino acids 1-42

### **N-glycosylation site.**

amino acids 2-6, 62-66, 107-111

### **Casein kinase II phosphorylation site.**

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

### **N-myristoylation site.**

amino acids 15-21, 74-80, 155-161

### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 27-38

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## FIGURE 123

GGGACTACAAGCCGCGCCGCTGCCGCTGGCCCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC  
TCCGGCTCTGCGCTCGGCTGCCTGACTTCTTCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC  
TCAAATCCAGCAATCGAACCCCAAGTGGTACAGGAATTTGAAAGTGTGGAACGTCTTGCATCATTACGGATTTCG  
AGACAAGTGACCCCAAGATCGAGTGAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTTTGACAACAAAA  
TTCAGGGAGACTTGGCGGGTCGTGCAGAAATACTGGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG  
ACTCAGCCCTTTATCGCTGTGAGGTCTGCTCGAAATGACCGCAAGGAAATTGATGAGATTGTGATCGAGTTAA  
CTGTGCAAGTGAAAGCCAGTGACCCCTGTCTGTAGAGTGCCGAAGGCTGTACCAGTAGGCAAGATGGCAACACTGC  
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCCTGCCACGGATT  
CCAGAGCCAATCCCAGATTTTCGCAATTTCTTTTCCACTTAAACTCTGAAACAGGCACTTTTGGTGTTCCTGCTG  
TTCACAAGGACGACTCTGGGCAGTACTACTGCATTGCTTCCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG  
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGGTTCTGGTTGTCCTTGCTGTACTGGCCCTGA  
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA  
ACCCAGGGAAACCAGATGAGTTAACTACATCCGCACTGACGAGGAGGGCGACTTCAGACACAAGTCATCGTTTTG  
TGATCTGAGACCCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTCAA  
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTTCAGAAGCTTTTTCGTTTTTGGCCAAAGTTGACCA  
CTACTCTTCTTACTCTAACAAGCCACATGAATAGAAGAATTTTCTCAAGATGGACCCGGTAAATATAACCACAA  
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTTCTTAATCTGTTTTCTGGCCTGATTCCCGCATGAGTATTAGG  
GTGATCTTAAAGAGTTTGCTCAGTTAAACGCCCGTGTGGGCCCTGTGAAGCCAGCATGTTTCACTGGTCTGTT  
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGGAACCCA  
GAAAAGGCTTCTTACACAGCAGCCTTACTTTCATCGGCCACAGACACCACCGAGTTTCTTCTTAAAGGCTCTGC  
TGATCGGTGTTGCACTGTCCATTGTGGAGAAGCTTTTGGATCAGCATTGTGTAACCAACCAAAATCAGGAAG  
GTAAATTGTTGCTGGAAGAGGGATCTTGCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA  
ACCTTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTTCTATGGGTCTTGTATTATTTTATAAAATTT  
TACATCTAAATTTTGTCTAAGGATGTATTTGATTATGAAAAGAAAATTTCTATTTAAACTGTAAATATATTGT  
CATACAATGTTAAATAACCTATTTTAAAGAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTAAAT  
TGGAAAATATCAATAATTAAAGATATTTTACCAAGGAATCCTCTCATGGAAGTTTACTGTGATGTTTCTTTTCT  
CACACAAGTTTTAGCCTTTTTTACAAGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT  
TAAAAATTCAGTTAAGCAATGTTGAAATCAGTTTGCATCTCTTCAAAAGAAACCTCTCAGGTTAGCTTTGAACT  
GCCTCTTCTTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACAGATG  
CCAGTCAGCTCCTGGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTTGCCCTCGCTGTCTGCCAGGAGGCCCT  
GCCATCCTTGGGCCCTGGCAGTGGCTGTGTCCCAGTGAGCTTTACTCACGTGGCCCTTGCTTTCATCCAGCACAGC  
TCTCAGGTGGGCACTGCAGGGACACTGGTGTCTTCCATGTAGCGTCCCAGCTTTGGGCTCCTGTAACAGACCTCT  
TTTTGGTTATGGATGGCTCACAAAATAGGGCCCCCAATGCTATTTTTTTTTTTAAGTTTGTTTAATTATTTGTT  
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAATAACATTTTTTAAAGAAAATGGAT  
CCCCTGTTCTCTTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTGCGATTTCAAAACAAACCATGAT  
GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAAGCTCAGGTGGAGCAGCCAGGTGAAAGGCCCTGGCGGGGAGGAAAAG  
TGAAAACGCTGAATCAAAAGCAGTTTTTCTAATTTTGAATTTTTCATCCGCCGGAGACACTGCTCCCATTT  
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTGTTCTTCAAGAGCAGGTGTTCTCAGCCTCACATGCCCT  
GCCGTGCTGGACTCAGGACTGAAGTGTGTAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCTGGA  
GAATGGCTCTCACTACTCACCTTGTCTTTTCACTTCCAGTGTCTTGGGTTTTTTTATACTTTGACAGCTTTTTTTT  
AATTGCATACATGAGACTGTGTTGACTTTTTTTAGTTATGTGAAACACTTTGCCGCAGGCCGCTGGCAGAGGCA  
GGAAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTGTCTGCTGCATGGCATCCTGGATGCTTAGCATGCAAGTTC  
CCTCCATCATTGCCACCTTGGTAGAGAGGGATGGCTCCCCACCTCAGCGTTGGGGATTACGCTCCAGCCTCCT  
TCTTGGTTGTCTAGTGTATAGGGTAGCCTTATTGCCCTCTTCTTATACCCTAAAACCTTCTACACTAGTGCCA  
TGGGAACCAGGTCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA  
CGGAAAAGGAATACTCGTGTATTTTAAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT  
GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTTGTTTAAAC  
CTCATTATATAAAGCTTCAAAAAACCCA

## **FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624

><subunit 1 of 1, 310 aa, 1 stop

><MW: 35020, pI: 7.90, NX(S/T): 3

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS  
PRIEWKKIQDEQTTYVFFDNKIQGDLGRAEILGKTSCLKIWNVTRRDSALYRCEVVARNDRK  
EIDEIVIELTVQVKPVTVPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA  
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDLNIGGIIGG  
VLVVLAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

**Important features of the protein:**

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 243-263

**N-glycosylation sites.**

amino acids 104-107, 192-195

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 107-110

**Casein kinase II phosphorylation site.**

amino acids 106-109, 296-299

**Tyrosine kinase phosphorylation site.**

amino acids 69-77

**N-myristoylation sites.**

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267